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The inheritance of rind color patterns and thirteen other traits in watermelon, Citrullus lanatus (Thunb.) Matsum. and Nakai

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The inheritance of rind color patterns and thirteen other traits in watermelon, *Citrullus lanatus* (Thunb.) Matsum. and Nakai

by

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INTRODUCTION

Citrullus lanatus (Thunb.), Matsum. and Nakai, commonly known as watermelon, is a vegetable that is widely grown for its fruit. In the United States, watermelon ranks 6th in total acreage and 16th in total value when compared with 22 principal vegetables grown in the United States (19). Even though extensive breeding programs have been developed to improve fruit quality and increase disease resistance, only 25 genes have been reported for watermelon.

This study was undertaken to determine the inheritance of mottled rind in watermelon. Mottled rinds are characterized by a rough surface texture since the light green areas are indented when compared to dark green areas. These observations lead to the assumption that the mottled parent, 75-11, produces a solid light green rind overlaid with areas of dark green tissue. However, free hand sections made of mottled watermelon rind show light green areas are superimposed over dark green tissue and covered with a waxy substance.

The seeds of 75-11, the mottled parent for this study, were given to Dr. Charles V. Hall by a farmer whose family had grown the melons for a number of years. The original source of the melon is not known. Besides the unusual mottled rind, 75-11 matures quickly, becoming ripe 28 days after fruit set, and has a high soluble solids reading indicating high sugar content. However, 75-11 does not possess good internal characteristics. Instead, 75-11 has a red-orange flesh color, a large amount of fiber, coarse flesh texture, and large dark brown seeds.

In an attempt to improve the internal characteristics of 75-11 while still maintaining the mottled rind and short maturation time, a cross was made between 75-11 and 'Supersweet'. 'Supersweet' is a commercially available sib-pollinated cultivar with pink flesh color, firm flesh texture, small dark brown mottled seeds, and a small amount of fiber. The initial cross was made in the field during the summer of 1975. The following year (75-11 x 'Supersweet') plants were grown and selfed in the field. The resulting seeds were used to start this study.

REVIEW OF LITERATURE

Fruit Weight

Weetman (21) found dominance for small fruit weight in a cross between small fruited and large fruited lines. Several genes appeared to be involved in the determination of fruit weight. Poole and Grimball (11) reported 25 genes were involved in F_2 segregation ratios for fruit weight and 12 genes were involved in the backcross population. Suzuki (18) found melon weight to be controlled by a single, incompletely dominant gene and at least four minor gene pairs.

Rind Color and Pattern

Weetman (21) found solid dark green rind to be dominant to solid light green. Variations in color, from light to medium green, found in the F_2 and backcross populations were attributed to the action of modifier genes. Porter (13) found dark green rind color was completely dominant to light green rind color in some crosses and incompletely dominant to others. Barham (1) determined that the yellow rind color in 'Royal Golden' was controlled by a single recessive gene. Warid and Abd-El-Hafez (20) found incomplete dominance for yellow skin color over green skin color in 'Yellow Skin'. 'Yellow Skin' melons are yellow colored during the entire developmental cycle while the rind of 'Royal Golden' turns yellow only at maturity.

Shimotsuma (16) reported that striped rind was dominant to solid-color rind and conditioned by a single gene. Weetman (21) found striping to be dominant in some crosses and recessive in others. Weetman suggested that the *D* or color locus might include a multiple allelic series that

includes an allele for striping. He proposed the symbols D for dark rind color, d^s for stripe, and d for light green color. Dark green would be dominant to both stripe and light green rind color. Stripe would be dominant to light green rind color. Another explanation of the data offered by Weetman was that the loci for stripe and rind color are separate but closely linked. Since close linkage would produce the same results as triple alleles, it was not possible to determine which was the correct explanation. Weetman also reported that another type of striping, pencil striping, was controlled by a single recessive gene. Pencil stripes are very narrow and inconspicuous. The symbol for this gene, p for penciled line, was assigned by Poole (10).

Weetman (21) reported that the greenish-white mottling found on the rind of 'Iowa Belle' was controlled by a single recessive gene. Poole (10) found the mottling on the cultivar 'Sun, Moon, and Stars' to be a cytoplasmically controlled trait. 'Sun, Moon, and Stars' has yellow spots on the leaves and fruit that lack chloroplasts. Mottling was seen only on the fruit of 'Iowa Belle'. Weetman (21) suggested that the gene controlling mottled rind was linked to the genes controlling dark rind color and the presence of stripes.

Robinson et al. (15) have suggested the use of the symbol G for the allele controlling dark rind color, g^s for stripe, and g for light green rind color. The suggested symbols for penciled stripe and mottled rind are p and m respectively.

Fruit Smoothness

Watermelon rinds are either smooth or grooved. Poole (10) reported that a single recessive gene, *f*, controls the presence of grooves. Therefore smooth rind is dominant to grooved rind.

Rind Thickness

Suzuki (18) suggests that a single pair of incompletely dominant genes control rind thickness. No symbol has been assigned to this gene.

Flesh Color

The flesh color of watermelon varies from white to yellow to pink to red. Two genes for yellow flesh have been studied. Porter (13) found that yellow flesh was recessive to red and was controlled by a single recessive gene, *y*. Poole (10) studied the gene for canary yellow flesh color and found it to be dominant to pink. Shimotsuma (16) studied a cross between red and white fleshed parents. The F_2 and backcross populations supported a digenic model for the control of flesh color. Poole (10) suggested a genetic notation of *Y* for yellow flesh and *W* for the epistatic gene for white flesh. This would result in *WY* being white, *Wy* being white, *wY* being yellow, and *wy* being red. Robinson, et al. (15) have suggested the symbol *Wf* for white flesh. No symbol has been assigned to the dominant gene for flesh color.

Seed Coat Color

Kanda (4) reported that seven pairs of alleles were involved in the determination of seed coat color in watermelon. However, Poole, Grimball, and Porter (12) suggest that Kanda's data was not in statistical agreement

with his suggested genetic model. McKay (6) found two independent genes were involved in the dominance of tan and green seed coat color over red seed coat color. Weetman (21) reported that the 'clump' phenotype, the presence of black bands on the edges of the seed, was recessive to the nonbanded pattern. The clump phenotype was controlled by one gene. Porter (13) found black seed coat color to be dominant to white seed coat color and was controlled by a single gene. He also found tan seed coat color to be dominant to white seed coat color. In addition, Porter (13) suggested that the black and tan seed coat colors were conditioned by two alleles. However, his data did not provide conclusive support for his digenic model. Nath and Dutta (8) reported tan seed coat color to be dominant to red seed coat color.

Poole, Grimball, and Porter (12) have suggested that three major genes, *R*, *T*, *W*, and one modifier gene, *D*, are involved in seed coat color. The three color genes interact to condition the various seed coat colors found: *RTW* is black, *RtW* is white tan tipped, *rtW* is red, *rtw* is white pink tipped, and *RTw* is clump which can be white black tipped. The phenotypes for *rTW* and *rTw* have not been encountered, but it has been suggested that *rTw* is green. The phenotype of *rTW* has not been suggested. The modifier gene, *D*, modifies only the black, *RTW*, genotype with *RTWD* being solid or flat black and *RTWd* being dotted or stippled.

The currently accepted seed coat color model is that proposed by Poole, Grimball, and Porter (12) involving the loci *R*, *T*, *W*, and *D*.

Total Soluble Solids

Suzuki (18) has determined that total soluble solids in watermelon are controlled by three incompletely dominant genes that are linked and by at least two minor genes.

Fruit Shape

Quantitative measures of fruit shape are obtained by calculating a length to diameter (LD) ratio. The LD ratio is obtained by dividing the length of the fruit measured between the blossom and stem ends by the diameter at the center of the fruit. Watermelons normally have one of three distinctive fruit shapes. The shapes are round, intermediate (blocky), and long. A round melon has an LD ratio of 1.00 to 1.25, an intermediate melon has an LD ratio of 1.25 to 1.75, and a long melon has an LD ratio greater than 1.75 (2).

Round melon shape has been found by McKay (6) to be dominant to long melon shape. Various researchers have reported round melon shape to be incompletely dominant to long melon shape (11, 16, 20, 21). In a quantitative study of fruit shape, Brar and Nandpuri (2) found that round melon shape was incompletely dominant to long melon shape in two of the three crosses they studied. They reported that there was no dominance in the third cross. Additive gene effects played a predominant role in the inheritance of fruit shape in all three crosses. The range in narrow sense heritability values was from 42.6 percent to 77.5 percent.

Current theory suggests that a single gene controls fruit shape and that round fruit shape is partially dominant to long. The suggested symbol for the fruit shape gene is *o* (10).

Seed Size

The size of watermelon seed can be measured by various methods. Length, weight, and volume have all been used as units of measure in genetic studies. Poole, Grimball, and Porter (12) reported that short (6mm) seeds and long (13mm) seeds were both recessive to medium (10mm) length seeds. Short and long seed lengths are controlled by single independent genes. Konsler and Barham (5), Shimotsuma (16), and Nath and Dutta (8) have all found medium length seeds (7.4mm - 8.8mm - 8.9mm) to be dominant to long length seeds (12.7mm - 12.8mm - 12.05mm). A single gene controls this difference in length. Poole, Grimball, and Porter (12) have assigned gene symbols of *s* for short seed length and *l* for long seed length. Observed F_2 ratios of 9(++):3 long (+*s*):4 short (*s*+ and *sl*) were found. Such data suggests the *s* gene is epistatic to the *l* gene.

Weetman (21) used the weight of 25 seeds as a measure of seed size. He found that one major dominant gene was responsible for light seed vs. heavy seed. However, his data did not fit a monogenic ratio so it is assumed that other factors are also involved in determining seed weight.

Suzuki (18) used the volume of 100 seeds as a measure of seed size. He found that a single pair of incompletely dominant genes along with at least three minor gene pairs in repulsion and one in coupling control seed size.

Days to Maturity

Suzuki (18) found that the number of days required for melons to mature was controlled by a single pair of completely dominant genes and at least three minor genes. Dominance was toward late ripening.

Linkage

Several investigators have reported on phenotypic correlation coefficients and linkage between various traits in watermelon. Weetman (21) suggested that linkage exists between a weight gene, the gene for mottled rind, *m*, and genes for rind color and stripe, *G*, g^s, and *g*. Weetman also reported a significant phenotypic correlation between fruit length and fruit weight. Time of maturity was significantly correlated with ovary shape ($r = -0.22$, $p = <0.01$), fruit length ($r = 0.46$, $p = <0.01$), and fruit width ($r = 0.29$, $p = <0.01$). He found a significant negative correlation between shape index (LD ratio) and fruit weight ($r = -0.23$, $p = <0.01$).

Poole, Grimball, and Porter (12) found no linkage between the four genes for seed coat color or the two genes for seed length. They did find linkage between *l* for long seeds and the color gene *G* with a linkage value of 19.3 ± 1.1 percent.

Poole (10) reported that fruit shape and fruit weight were significantly correlated ($r = -0.31$, $p = <0.01$). Porter (13) looked for linkage between the following traits and found none: flesh color and seed size, flesh color and skin color, fruit skin color and rind toughness, rind toughness and seed coat color, rind toughness and flesh color, and fruit skin color and seed coat color.

Suzuki (18) found highly significant phenotypic correlation between fruit weight and rind thickness ($r = 0.69$, $p = <0.01$), fruit weight and rind toughness ($r = 0.65$, $p = <0.01$) and rind thickness and rind toughness ($r = 0.59$, $p = <0.01$). Significant phenotypic correlations were found for fruit weight and leaf number ($r = 0.05$, $p = 0.05$), total solid and rind thickness ($r = .0992$, $p = 0.05$), and for seed size and rind toughness ($r = 0.025$, $p = 0.05$).

MATERIALS AND METHODS

Procedures

The original source of the mottled rind color character used in this study is unknown. A farmer gave Dr. C. V. Hall some watermelon seed which, when planted, produced the mottled melon referred to in this paper as 75-11. The characteristics of 75-11 are found in Table 1. 75-11 also has a short, 28 day, maturity period. In an attempt to improve the internal characteristics of 75-11 while still maintaining the mottled rind color and short maturation time, a cross was made between 75-11 and 'Supersweet'. 'Supersweet' is a commercially available sib-pollinated cultivar whose characteristics are listed in Table 1. The initial cross was made in the field during the summer of 1975. The following year F_1 plants were grown and selfed in the field. Seeds from these plants were used to start this study.

During the summer of 1977 a small population, 32 plants, of (75-11 x 'Supersweet') F_2 was grown. Observations from this population indicated that a larger population would be needed to determine the inheritance of mottled rind color since no 'Supersweet' rind color phenotypes were recovered. The range of phenotypes found in the F_2 population also suggested that this cross would not easily indicate the inheritance of mottled rind color since the striped character in 'Supersweet' seemed to confound the discrete classification of mottled and nonmottled phenotypes.

Additional crosses with 75-11 were made in the greenhouse during the winter of 1977-78 in an attempt to find populations with background colors and rind color patterns which would produce distinct mottled and

Table 1. The phenotypic characters of ten watermelon cultivars used in a genetic study of mottled rind color

Cultivar	L/D	Shape	Rind Color			Flesh		Seed	
			Background	Stripe	Net	Color	Texture	Color	Size
Charleston Gray	3.0	Oblong	Light green	None	Dark green	Red	Firm	Dark brown mottled	Medium
Congo	2.0	Oblong	Dark green	Very dark green	None	Red	Medium	Tan	Medium
Sugar Baby	1.0	Round	Dark green	Very[a] dark green	None	Red	Firm	Dark brown mottled	Small
Winter Queen	1.0	Round	Greenish white	Light green	None	Red	Firm	Black	Small
Klondike	3.0	Oblong	Light green	Dark green	None	Red	Firm	White-black tips	Medium
Desert King	1.0	Round	Light green	None	None	Yellow	Firm	Dark brown mottled	Large
Golden Midget	1.0	Round	Medium green[a] to yellow	Dark[a] green	Dark[a] green	Red	Firm	Black	Small
Stone Mountain	1.0	Round	Medium green	None	Dark green	Red	Firm	White-black tip	Large

75-11	1.0	Round	Light green	Medium green mottled	None	Orange Red	Coarse	Dark brown mottled	Large
Supersweet	1.0	Round	Light green	Dark green	Dark green	Red	Very firm	Dark brown mottled	Small

[a]Observed in immature melons only.

nonmottled phenotypes. Watermelon cultivars used in these crosses are listed in Table 1. Reciprocal crosses were also made between 75-11 and 'Supersweet'. Original (75-11 x 'Supersweet') F_1 seeds from 1975 were planted to produce F_2 and backcross populations.

Plants were grown in 10 inch (25.4 cm) clay pots containing a soil mix of one part soil, one part peat, and one part perlite. Three plants were grown in each pot. 75-11, 'Supersweet', and (75-11 x 'Supersweet') F_1 populations were seeded on October 11, 1977. Additional cultivars were seeded on Dec. 10, 1977. The plants were grown under 12 hours of artificial light until the vines needed to be trained. Training support was provided by tying string under the rim of the pot and attaching it to wires running above the benches. Plants were attached to the strings with twistems. Temik was used at recommended rates to control thrips. Plants were fertilized weekly with a solution of 20-20-20 Peter's fertilizer at a rate of 2 lb/100 gal (0.24 kgm/100 l).

Hand pollinations were made using the appropriate cultivars as male or female parents to obtain the crosses listed in Table 2. Pollen was placed on the stigma of female flowers as soon after the female flower opened as possible. This was done by removing newly opened male flowers with dehiscent anthers from the appropriate plant, removing the petals, and then rubbing the anthers on the stigmatic surface of appropriate styles to insure an adequate amount of pollen was transferred. After pollination, a tag with the date and information about the cross was hung on the female flower. No attempt was made to control contamination from outside pollen sources since the average outdoor temperature of 15°F (-6°C) during this period should eliminate external insect activity.

Watermelons were harvested 60 days after pollination. Seeds were removed, washed, and dried soon after the melons were harvested.

During the summer of 1978, populations produced from these crosses were grown under commercial conditions at the Iowa State University Horticulture Research Station near Gilbert, Iowa (Table 2). Seeds were sown during the week of May 1 in 2¼ in. (5.7 cm) diameter peat pots that had been placed in greenhouse flats. The soil mix used was similar to that previously described. Flats of pots were placed in a greenhouse with an average temperature of 90°F (32.2°C) until the seeds had germinated. Flats were then moved to a greenhouse with a temperature of 65°F (18.3°C). On May 17 the plants were transplanted to the field.

Prior to transplanting, fields were plowed and disked. Fertilizer was applied at a rate of 10 lb (4.5 kgm) of 15-15-15 per 100 feet (35.5 m) of row. The fields were also marked to produce a grid of six feet (1.8 m) between rows and six feet (1.8 m) between plants. Individual melon populations were planted in blocks with no replication since the main emphasis of this study was to determine the inheritance of qualitative traits.

A starter solution was used containing 6.25 lb/100 gal (7.5 g/l) of methoxychlor 50 WP and 3.13 lb/100 gal (3.25 g/l) of 15-30-15 Peter's fertilizer at transplanting. Approximately 1 cup (250 ml) of this solution was applied per plant. The first insecticide application was made 2 days after transplanting (May 19) when considerable damage, due to cucumber beetles, *Aclymma vittata* and *Diabrotica undecimpumctat howardi*, was observed. The plants were sprayed weekly through the entire growing season with 6.25 lb/100 gal (7.5 g/l) of methoxychlor 50 WP to provide protection from cucumber beetles.

Table 2. 1978 watermelon populations

Population	Population Size
75-11	38
Supersweet	25
Supersweet x 75-11	24
75-11 x Supersweet	18
(75-11 x Supersweet) F_2	223
75-11 x (75-11 x Supersweet)	213
(75-11 x Supersweet) x 75-11	6
Supersweet x (75-11 x Supersweet)	110
(75-11 x Supersweet) x Supersweet	130
Desert King	4
Desert King x 75-11	4
Charleston Gray	5
Charleston Gray x 75-11	6
Golden Midget	4
Golden Midget x 75-11	5
Stone Mountain	5
Stone Mountain x 75-11	6
Sugar Baby	3
Sugar Baby x 75-11	6
Winter Queen	3
Winter Queen x 75-11	6
Klondike	4
Klondike x 75-11	6
Congo	3
Congo x 75-11	5
Golden Honey	4
Golden Honey x 75-11	4

A short time after fruit set each melon was tagged to indicate the approximate date of fruit set. One melon from each plant was harvested for evaluation. The melons were harvested when they were thought to be ripe as evidenced by the number of days from fruit set and by the color of the ground spot. Beginning 28 days from fruit set, melon ground spots were examined. When the appropriate ground spot color was observed, the melon was harvested. An individual plant code was recorded on each melon. The ground spot is the area of the rind that is in contact with the ground. The color of the ground spot changes as the melon matures and may vary with rind color. Dark green melons, such as 75-11, possess a bright yellow ground spot at maturity while melons with a light green background, such as 'Supersweet', possess light yellow ground spot with brown veins at maturity. Since Nip, Burns, and Paterson (9) have shown that the color of the ground spot was significantly correlated to the color and sweetness of the fruit ($r = 0.99$). Melons on 75-11 plants mature in approximately 28 days while 'Supersweet' melons mature in 35 to 40 days (Dr. C. V. Hall, Department of Horticulture, Iowa State University, Ames, Iowa, personal communication).

Melon populations were evaluated for the quantitative and qualitative traits listed in Table 3. Immediately after harvest melons were evaluated for the following traits.

Harvest date The harvest date was the date the melon was harvested using the criteria previously described for ripeness. A numerical value indicating the month and the day of the month was recorded, for example, June 22 would be recorded as 0622.

Table 3. Characteristics evaluated in 1978 watermelon populations

Quantitative traits	Qualitative traits
Harvest date	Rind mottle
Approximate date of fruit set	Rind stripe
Melon weight	Rind color
Melon length	Rind smoothness
Melon width	Flesh color
Rind thickness	Flesh texture
Percent soluble solids	Flesh fiber
Mean seed weight	Seed color
	Ripeness

Approximate date of fruit set The approximate date of fruit set was written on a tag and attached to each melon. This data was recorded similar to harvest date.

Melon weight Each melon was weighed by placing the melon in a basket attached to a scale suspended from a tripod. Melon weights were recorded to the nearest tenth of a pound.

Melons were also evaluated for 11 traits that comprise their external phenotype.

Mottle Each melon was classified as being either mottled or nonmottled. Small parts of mottled melon rind appear sunken in relation to the epidermis. The sunken areas are characterized by a waxy appearance (Figure 1).

Stripe Each melon was classified as being striped or nonstriped.

Rind color Rind color was broken down into four parts, background color, stripe color, mottle color, and netting color. The color of each of these melon traits was recorded as being either white, cream, yellow,

Fig. 1. 75-11

Fig. 2. 'Supersweet'

light green, medium green, dark green, or black. Background color was considered to be the lightest color present for striped melons, however, in mottled melons the background color was recorded as the predominant color of the melon. Stripe color was recorded as the darkest color present on striped melons. Mottle color was the color of the indented areas on mottled melons. The color of any netting found on the melon was recorded.

Smoothness Each melon was classified as being either smooth or grooved. A grooved melon has long longitudinal indentations in the rind that do not follow placental lines since melons with more than six grooves were observed. Each appears to be associated with a vascular bundle that lies immediately beneath it.

After the melons were evaluated for external phenotypic traits the melons were cut in half from blossom to stem end. The melons were then evaluated for the following internal characteristics:

Melon length The length of each melon was found by measuring the distance between the blossom and stem ends. Measurements were recorded in millimeters.

Melon width The diameter of each melon was measured at a point midway between the blossom and stems. Melon width was measured in millimeters.

Rind thickness Rind thickness was measured in millimeters midway between the melon's blossom and stem ends. The mean of two measures was recorded.

Flesh color The flesh of each melon was visually examined and subjectively rated. Flesh was classified as being white, yellow, pink, pink-orange, orange, orange-red, or red.

Flesh texture The flesh texture of each melon was visually examined and rated subjectively. Texture was based on the compactness of the cells in the flesh. Flesh textures were recorded as being very fine, fine, medium, or coarse.

Flesh fiber Each melon was visually examined to determine if there were large amounts of placental fiber present. Flesh fiber was classified as being either absent or present.

Seed color The color of seeds in each melon was recorded. Categories used for seed color were: white or tan, white with black tip, yellow, dark brown mottled, black, or black stripe.

Percent soluble solids Percent soluble solids were measured by placing a few drops of juice from the heart of each melon on an American Optical hand held refractometer. Measurements were recorded in tenths of a percent with no temperature compensation. Showalter (17) found a very high correlation coefficient ($p = 0.96$-0.98) between the solids found in subsamples of a watermelon and that found in the entire edible flesh. He concluded that since the distribution of soluble solids in watermelons was very consistent, the percent soluble solids tested in one area provides a good indication of the soluble solids of the entire flesh. Porter et al. (14) compared soluble solids measurements from the center of the melon with those from the entire fruit. They found the largest difference in the two values to be 0.4 percent. They concluded that two or three drops of juice from the center of a ripe melon gave approximately the same

refractometer readings as a composite sample taken from the melon. Porter et al. (14) stated that a hand held refractometer was an acceptable means of determining the sweetness of a watermelon since the trends for soluble solids and total sugars are similar. About 85 percent of the total soluble solids are sugars. Nip, Burns, and Paterson (9) also found a significant correlation beteeen the sweetness of melons and percent soluble solids ($r = 0.98$, $p = 0.01$).

Ripeness All melons were classified as being under-ripe, ripe, or over-ripe. Under-ripe melons had the distinctive sour taste associated with under-ripe melons. Some under-ripe melons exhibited poor internal flesh color development. Over-ripe melons were characterized by flesh texture breakdowns.

Mean seed weight A sample of seeds was removed from each melon. The seeds were washed and allowed to air dry. After all of the seeds were dry, 50 seeds from each melon were weighed. Weights were recorded in grams. Mean seed weight was calculated by dividing the weight recorded by 50.

The traits days to harvest, maturity index, length diameter (LD) ratio, and melon density were calculated from other traits previously described.

Days to harvest The number of days to harvest was determined by subtracting the Julian date at planting from the Julian date at harvest.

Maturity index The maturity index was found by subtracting the Julian date for fruit set from the Julian date for the day of harvest. Maturity index provides a measure of the number of days required for melons to mature.

Length diameter (LD) ratio The length diameter ratio was found by dividing the length of the melon by the width of the melon. LD ratios are used as an indicator of fruit shape since round melons produce an LD ratio of 1.00-1.25, block melons produce an LD ratio of 1.25-1.75 and oblong melons produce LD ratios greater than 1.75 (2).

Melon density The density of each melon was found by dividing the mass of the melon by its volume. The mass in grams of the melon was found by multiplying its weight in pounds by a conversion factor of 453.6 grams per pound. The volume was found by using the formula for the volume of a prolate spheroid, $V = \frac{4}{3}\pi AB^2$. In this formula A was the major axis (length), and B was the minor axis (width). Density was recorded in grams per cubic centimeter.

Genetic models were tested by using chi-square tests to determine if the observed values were in agreement with the expected value. Orthogonal contrasts as described by Elandt-Johnson (3) were used to divide the chi-square values found in tests for independence into component parts. The contrast for linkage was used to determine if linkage was used to determine if recombination did occur in the expected amounts. The means of various genetic populations were compared using a t-test to determine if the means were significantly different. The populations were considered to be independent samples and a pooled estimate of variance also was used to account for varying population sizes. Means were considered to be significantly different if the probability of the t value was 0.05 or less.

RESULTS AND DISCUSSION

The traits listed in Table 3 will be discussed in order. It should be noted that these traits begin as external characters and proceed to describe internal traits. Traits derived by combining other traits will be discussed last.

Fruit Weight

In a cross between light weighted and heavy weighted melon cultivars, Weetman (21) found light melons were dominant. The data suggest several genes are involved in the inheritance of melon weight. Research by Poole and Grimball (11) suggests that 25 genes were required to explain the observed segregation of an F_2 population and that 12 genes were required to explain the backcross ratios produced. In this study light weight melons were also dominant to heavy weight melons. Suzuki (18) found light melon weight to be controlled by five loci, one single incompletely dominant gene with four modifiers.

In this study the mean fruit weight of 75-11 melons was 19.0 lb (8.6 Kg) (Table 4). 'Supersweet' produced melons with a mean weight of 17.6 lb (8.0 Kg). Mean melon weights for the two parental populations are not significantly different at the five percent level using a t-test comparison. F_1 populations of ('Supersweet' x 75-11) and (75-11 x 'Supersweet') produced mean melon weights of 21.5 lb. (9.5 Kg) and 16.9 lb. (7.7 Kg) respectively. When the two F_1 population means were compared by a t-test the results suggest there is a significant difference between the means of the two populations ($p = 0.01$). The (75-11 x 'Supersweet') population mean was not significantly different from the

Table 4. Distribution of watermelon weight in percent, for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Melon weight in pounds Upper limit of class 9.9	14.9	19.9	24.9	29.9	34.9	Mean
75-11 (P_1)	38	3	12	50	23	12		19.0 ± 4.0
Supersweet (P_2)	25	4	20	48	24		4	17.6 ± 4.5
($P_2 \times P_1$)	24			40	36	16	8	21.5 ± 4.4
($P_1 \times P_2$)	18		33	28	33	6		16.9 ± 4.5
($P_1 \times P_2$) F_2	223	5	30	44	19	1	1	16.4 ± 4.2
$P_1 \times (P_1 \times P_2)$	213	3	18	36	34	8	1	18.7 ± 4.7
$(P_1 \times P_2) \times P_1$	6		17	49	34			19.8 ± 3.8
$P_2 \times (P_1 \times P_2)$	110	1	11	37	39	9	3	20.0 ± 4.3
$(P_1 \times P_2) \times P_2$	130		1	20	45	32	3	18.5 ± 4.1

population means of either 75-11 or 'Supersweet' ($p = 0.10$, $p = 0.50$). The ('Supersweet' x 75-11) F_1 population mean value was not significantly different from the mean value of the 75-11 population ($p = 0.08$), but it was significantly different from the mean value of the 'Supersweet' population ($p = 0.001$).

There was no difference between the F_1 population (75-11 x 'Supersweet') mean of 16.9 lb (7.7kg) and its F_2 population mean of 16.4 lb (7.5kg), when compared by t-test at the five percent level. In addition, the F_2 mean did not differ significantly from either the mid-parent mean or the geometric mean which were both 18.3 lb (8.3kg; $p = 0.10$). The F_2 population mean was significantly different from the 75-11 population mean of 19.0 lb (8.6kg; $p = 0.001$) but was not significantly different from the 'Supersweet' population mean of 17.6 lb (8.0kg; $p = 0.20$).

Although the mean values of both the (75-11 x 'Supersweet') F_2 and F_2 populations were smaller than the population mean of the smallest parent, 'Supersweet', none of the means were significantly different. Light weight melons appear to be dominant. Transgressive segregation also occurs in these populations. Using the mean value of the 75-11 population and a pooled variance for both the 75-11 and (75-11 x 'Supersweet') F_2 populations, the smallest mean value for the F_2 population that would not be significantly different at the 5 percent level was found. The value produced was 17.7 lb (8.0kg). Sixty-nine percent of the F_2 population weighed less than this value. If the F_2 population is divided into two groups using 17.7 lbs as a dividing point, the observed data do not fit well ($p = 0.05$) the 3:1 model expected if one gene controls light melon weight.

Weetman (21), Poole and Grimball (11), and Suzuki (18) have all found light melon weight to be dominant. The results of this study agree with those findings

Mean melon weights produced from crosses between other commercial cultivars and 75-11 are found in Table 5. 'Golden Midget' (4.5 lb, 2.0kg) is much smaller than 75-11 (19.0 lb, 8.6kg). The F_1 population of 'Golden Midget' x 75-11 produced melons with a mean weight of 12.8 lb (5.8kg). 'Stone Mountain' produced melons with a mean weight of 32.4 lb (14.7kg). The F_1 population, 'Stone Mountain' x 75-11, produced melons with a mean weight of 28.7 lb (12.0kg). Both of these examples suggest additive gene action controls mean watermelon weight. The remaining cultivars and F_1 populations produced mean melon weights similar to those of 75-11.

Rind Color and Pattern

The three traits that constitute the primary external phenotype of watermelons produced for this study are rind color, striping, and rind mottling. These three traits will be discussed individually, then as groups of two, and finally as a composite group. Within each discussion, data from 75-11 x 'Supersweet' populations as well as data from half-sib related populations of commercial watermelon cultivars and 75-11 will be used to illustrate genetic relationships.

Rind color

Weetman (21) suggests that one dominant gene is responsible for the rind color of watermelon. He classified F_2 populations into dark, medium, and light green rind color phenotypes. When testing the genetic model both the medium and light green classes were bulked to form a light green

Table 5. Mean melon weights of commercial watermelon cultivars and F_1 populations grown in 1978

Plant population	No. of plants	Mean weight in pounds
75-11	39	19.0 ± 4.0
Desert King	4	21.9 ± 3.5
Desert King x 75-11	4	22.8 ± 1.8
Charleston Gray	5	25.5 ± 8.3
Charleston Gray x 75-11	6	23.6 ± 3.1
Golden Midget	4	4.5 ± 1.2
Golden Midget x 75-11	5	12.8 ± 0.9
Stone Mountain	5	32.4 ± 12.6
Stone Mountain x 75-11	6	28.8 ± 7.7
Sugar Baby	3	15.4 ± 1.3
Sugar Baby x 75-11	6	14.6 ± 2.8
Winter Queen	3	15.9 ± 2.6
Winter Queen x 75-11	6	16.4 ± 2.1
Klondike	4	20.1 ± 3.9
Klondike x 75-11	6	20.0 ± 3.5
Congo	3	21.1 ± 3.8
Congo x 75-11	5	24.8 ± 3.2
Golden Honey	4	16.2 ± 2.8
Golden Honey x 75-11	4	14.9 ± 3.8

class for chi-square tests. Weetman also suggested that the color locus has three alleles: G for solid dark green, g^s for stripe, and g for solid light green. Solid dark green melons would be dominant to striped and solid light green melons; striped melons would be dominant over solid light green melons. Porter (13) stated that crosses between light green and dark green melons result in dark green color being completely dominant in some crosses and incompletely dominant in others. Both Barham (1) and Warid and Abd-El-Hafez (20) found green rind color to be dominant to yellow rind color.

In this study the mottled parent, 75-11, is a nonstriped melon with a dark green mottled rind (Fig. 1). 'Supersweet' is a striped melon with broad dark green stripes on a very light green background (Fig. 2). 75-11 will be classified as a dark green melon for this trait. Field grown F_1 populations resulting from crosses between 75-11 and 'Supersweet' produced two phenotypes, melons which were solid dark green and others which were medium green with dark green stripes (Figs. 3 and 4). The F_1 plant (75-11 x 'Supersweet'), used to create the F_2 and backcross populations was not grown in the field, however, F_1 winter grown greenhouse melons were medium green with stripes. F_2 melons were classified as having either dark, medium, or light green background color. There were 64 melons with dark green background color, 113 melons with medium green background color, and 48 melons with light green background color (Table 6). Backcross populations were also classified according to background color (Table 6).

Since Weetman (21) grouped light and medium green melons together and considered them to be light green, F_2 melons from this study were first

Fig. 3. 75-11 x 'Supersweet'

Fig. 4. 75-11 x 'Supersweet'

Table 6. Distribution of rind background color in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Rind background color — Observed — Dark green	Medium green	Light green	— Expected[a] — Dark green	Medium green	Light green	Model	X^2	P
75-11 (P_1)	39	100	0	0	100	0	0			
Supersweet (P_2)	25	0	0	100	0	0	100			
(P_2 x P_1)	24	58	42	0	0	100	0			
(P_1 x P_2)	22	45	55	0	0	100	0			
(P_1 x P_2) F_2	223	29	51	21	25	50	25	1:2:1	2.96	0.23
P_1 x (P_1 x P_2)	213	78	22	0	50	50	0	1:1:0		
(P_1 x P_2) x P_1	6	50	50	0	50	50	0	1:1:0		
P_2 x (P_1 x P_2)	110	0	64	36	0	50	50	0:1:1		
(P_1 x P_2) x P_2	130	0	49	51	0	50	50	0:1:1		

[a]Expected ratio if the intensity of watermelon rind background color is controlled by one incompletely dominant gene (1:2:1).

Table 7. Distribution of rind background color in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Rind background color: Observed Dark green	Observed Light green	Expected[a] Dark green	Expected[a] Light green	Model	X^2	P
75-11 (P_1)	39	100	0	100	0			
Supersweet (P_2)	25	0	100	0	100			
($P_2 \times P_1$)	24	58	42	100	0	1:0		
($P_1 \times P_2$)	22	45	55	100	0	1:0		
($P_1 \times P_2$) F_2	223	27	73	75	25	3:1	254.9	<0.001
$P_1 \times (P_1 \times P_2)$	213	78	22	100	0	1:0		
$(P_1 \times P_2) \times P_1$	6	50	50	100	0	1:0		
$P_2 \times (P_1 \times P_2)$	110	0	100	50	50	1:1	55	<0.001
$(P_1 \times P_2) \times P_2$	130	0	100	50	50	1:1	65	<0.001

[a]Expected ratios if the intensity of watermelon rind background color is controlled by a single completely dominant gene, (3:1).

classified in this manner. Data show poor fit ($p = <0.001$) to Weetman's (21) genetic model (Table 7).

Using a genetic model of incomplete dominance for dark green background color, a ratio of 1 dark green:2 medium green:1 light green would be expected. The F_2 data fit ($p = 0.23$) this model producing a chi-square value of 2.96 (Table 6). Two backcross populations ((75-11 x 'Supersweet') x 75-11) and ((75-11 x 'Supersweet') x 'Supersweet') agree with the expected genetic models of 1:1:0 and 0:1:1 respectively. The (75-11 x (75-11 x 'Supersweet')) population produced an excessively large proportion of dark green melons which did not agree with the proposed genetic model. This backcross population was sorted into three groups: mottled, nonmottled solid dark green, and nonmottled medium green with a dark green stripe. Melons that were classified as mottled were classified as dark green. It is possible that closer examination of the mottled group could have lead to further classification by background color. The ('Supersweet' x (75-11 x 'Supersweet)) population does not agree with the expected values. The medium green group was larger than expected.

F_1 melons used to create F_2 and backcross populations provide support for the incomplete dominance of dark green rind color, however, the presence of solid dark green melons in F_1 field populations does not support the incomplete dominance of light green rind color. Since a population of (75-11 x 'Supersweet') F_2 created by field selfing an original (75-11 x 'Supersweet') F_1 plant failed to segregate and another F_2 population derived from a greenhouse grown F_2 seed did segregate the purity of the parent seed lots are suspect.

Classification of both F_1 populations into two phenotypes suggests that the F_1 phenotype is not uniform. The two phenotypes may have been produced because the parents were not homozygous or the pollen may have been contaminated. To adequately determine the cause of this problem, 75-11 should be grown and control selfed for at least one generation to determine if the line is homozygous and determine if the seed source is pure.

The mottled parent, 75-11, was crossed to ten commercially available cultivars (Table 1). Dark green rind color of 75-11 was completely dominant to yellow-white rind color of 'Desert King' (Figs. 5 and 6), the yellwo rind of 'Golden Midget' (Figs. 7 and 8), the light green rind color of 'Stone Mountain' (Figs. 9 and 10), and the medium green rind color of both 'Golden Honey' and 'Congo' (Figs. 11 and 12). The dark green rind color of 75-11 was incompletely dominant to the light green rind color of 'Charleston Gray' (Figs. 13 and 14) and the yellow-white rind color of both 'Winter Queen' (Figs. 15 and 16) and 'Klondike' (Figs. 17 and 18, Table 8). Although one dominant gene is involved, the degree of dominance varies from incomplete to complete dominance. Incomplete dominance may be triggered by the action of modifier genes in some cultivars which allow the expression of the heterozygous medium green phenotype.

Striping

Both McKay (6) and Shimotsuma (16) have reported that striping is controlled by a single dominant gene. However, Weetman (21) found striping to be a dominant character in some crosses and a recessive character in others. Weetman suggests that the factor for striping could be one

Fig. 5. 'Desert King'

Fig. 6. 'Desert King' x 75-11

Fig. 7. 'Golden Midget'

Fig. 8. 'Golden Midget' x 75-11

Fig. 9. 'Stone Mountain'

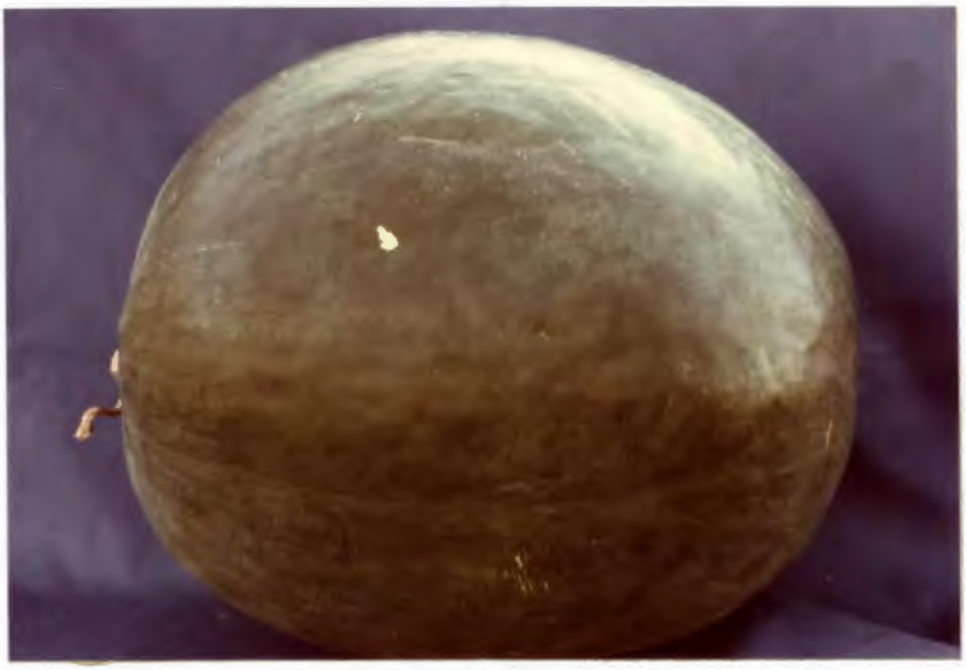

Fig. 10. 'Stone Mountain' x 75-11

Fig. 11. 'Congo'

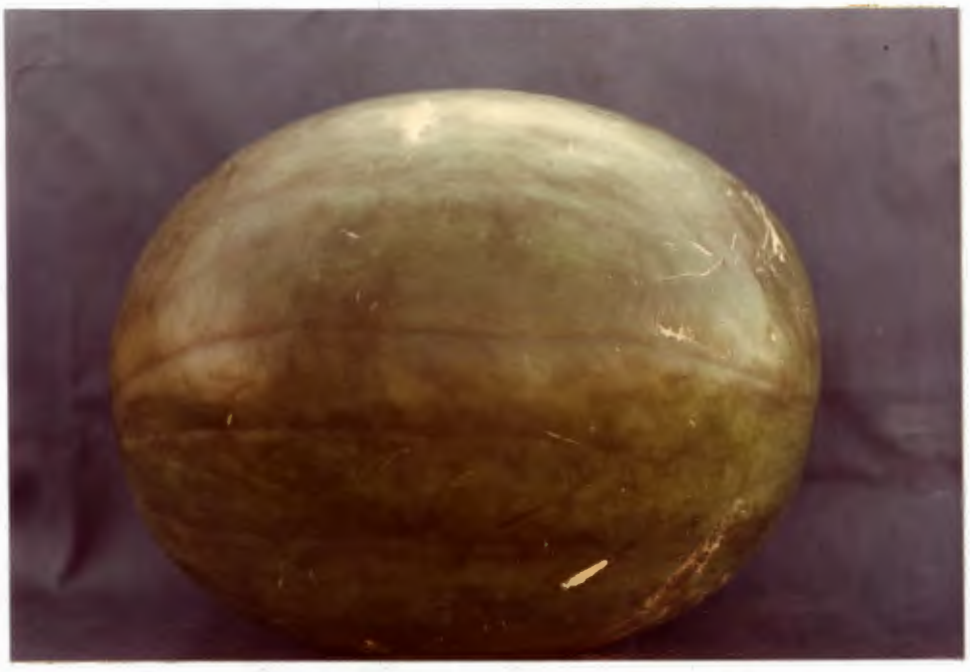

Fig. 12. 'Congo' x 75-11

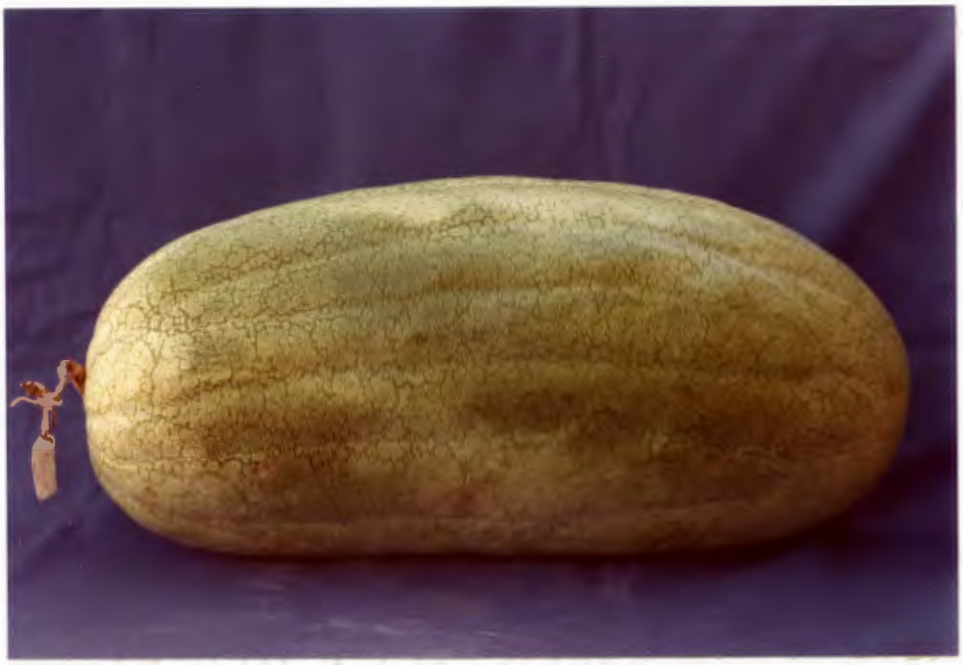

Fig. 13. 'Charleston Gray'

Fig. 14. 'Charleston Gray' x 75-11

Fig. 15. 'Winter Queen'

Fig. 16. 'Winter Queen' x 75-11

Fig. 17. 'Klondike'

Fig. 18. 'Klondike' x 75-11

Table 8. Rind color phenotypes of commercial watermelon cultivars and F_1 populations grown in 1978

Plant population	Watermelon background color	Degree of dominance
75-11	dark green	
Desert King	very light green	
Desert King x 75-11	dark green	complete
Charleston Gray	light green	
Charleston Gray x 75-11	medium green	incomplete
Golden Midget	immature - light green mature - yellow	
Golden Midget x 75-11	dark green	complete
Stone Mountain	light green	
Stone Mountain x 75-11	dark green	complete
Sugar Baby	dark green	
Sugar Baby x 75-11	dark green	---
Winter Queen	yellow-white	
Winter Queen x 75-11	medium green	incomplete
Klondike	yellow-white	
Klondike x 75-11	medium green	incomplete
Congo	medium green	
Congo x 75-11	dark green	complete
Golden Honey	medium green	
Golden Honey x 75-11	dark green	complete

allele of a multiple allelic series at the *G* color locus. In this genetic model the g^s allele for striping would be dominant to the *g* allele for solid light color and recessive to the *G* allele for solid dark green color. Weetman also has proposed a second genetic model which suggests that the locus for striping is different, but closely linked to the color locus. He also reported that pencil stripes, very narrow and inconspicuous stripes, were conditioned by a single recessive gene that was inherited independently of the g^s allele.

The mottled parent 75-11 (Fig. 1), is a nonstriped melon while 'Supersweet' (Fig. 2) is striped. Reciprocal F_1 populations from crosses between these two parents produced two phenotypes, melons that were solid dark green and others that were medium green with darker stripes (Figs. 3 and 4). The F_1 plants used to obtain (75-11 x 'Supersweet') F_2 and backcross populations produced medium green melons with darker stripes. F_2 melons were placed in one of two groups, striped or nonstriped. The observed segregation ratio of 169 striped:54 nonstriped fit ($p = 0.73$) a 3:1 model of 167:56 (Table 9). The 3:1 model suggests that the presence of one dominant allele for stripe in the plant genotype conditions the production of striped melons.

The only backcross population that does not fit expected ratios is (75-11 x (75-11 x 'Supersweet')) (Table 9). This population was separated into three groups: mottled, solid dark green, and medium dark green with a dark green stripe. The mottled group was considered nonstriped. An additional phenotype, stripes on a mottled background was found in the F_2 population but not in this backcross population. Melons in the mottled group were not closely examined to determine if striping was present.

Table 9. Distribution of stripe phenotype in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Striped melon phenotype — Observed — Stripe	Nonstripe	— Expected[a] — Stripe	Nonstripe	Model	X^2	P
75-11 (P_1)	39	0	100	0	100			
Supersweet (P_2)	25	100	0	100	0			
(P_2 x P_1)	24	50	50	100	0	1:0		
(P_1 x P_2)	22	50	50	100	0	1:0		
(P_1 x P_2) F_2	223	76	24	75	25	3:1	0.12	0.73
P_1 x (P_1 x P_2)	213	23	77	50	50	1:1	89.70	<0.001
(P_1 x P_2) x P_1	6	50	50	50	50	1:1	0.00	1.00
P_2 x (P_1 x P_2)	110	100	0	100	0	1:0		
(P_1 x P_2) x P_2	130	100	0	100	0	1:0		

[a]Expected ratios if stripes are controlled by a single dominant gene, (3:1).

Closer examination of the backcross population might provide data for this phenotype.

The mottled parent, 75-11, was crossed to ten commercially available sib-pollinated watermelon cultivars (Table 1). The parents and resulting F_1 populations were phenotypically classified as being either striped or nonstriped (Table 10). Parents with distinct stripes yielded F_1's with distinct stripes. However, 'Sugar Baby' which produces stripes in its immature state and solid green melons when mature produced different results. Progeny from the cross, 'Sugar Baby' x 75-11, produced a dark green melon with no stripes irrespective of maturity. 'Golden Midget' (Figure 7) has stripes that are veins of a darker shade of green when immature and yellow when mature. Progeny from the cross 'Golden Midget' x 75-11 (Figure 8) did not show any striping. 'Golden Midget' stripes may be pencil stripes reported by Weetman (21) to be recessive to solid dark green.

Data from crosses made between commercial watermelon cultivars and 75-11 suggest that striping is dominant to solid color. These results agree with those found by McKay (6) and Shimotsuma (16). They suggest striping is a dominant trait.

Mottling

Weetman (21) has determined that the inheritance of mottled rind in watermelon is controlled by a single recessive gene. The cultivar used as the mottled parent for this study was 'Iowa Belle'. In a cross between 'Iowa Belle' and a nonmottled parent, 'Japan 6', the F_1 melons produced were inconspicuously mottled. The semi-mottled appearance was

Table 10. Striped and nonstriped phenotypes of commercial watermelon cultivars and F_1 populations grown in 1978

Plant population	Stripe phenotype	
	Striped	Nonstriped
75-11		X
Desert King		X
Desert King x 75-11		X
Charleston Gray		X
Charleston Gray x 75-11		X
Golden Midget	X[a]	
Golden Midget x 75-11		X
Stone Mountain		X
Stone Mountain x 75-11		X
Sugar Baby	X[b]	
Sugar Baby x 75-11		X
Winter Queen	X	
Winter Queen x 75-11	X	
Klondike	X	
Klondike x 75-11	X	
Congo	X	
Congo x 75-11	X	
Golden Honey		X
Golden Honey x 75-11		X

[a]Stripe classified as a darker vein of the background color.

[b]Stripes visible on immature fruit but not on mature melons.

possibly caused by the partial expression of the mottled character. The F_2 population did not provide good fit to a 1:2:1 genetic model; however, when the semi-mottled and mottled groups were combined a perfect 3:1 ratio was observed. Crosses made to other nonmottled cultivars produced F_2 frequencies that agreed with 3:1 ratios. Weetman (21) suggested that genes were present in 'Japan 6' that were capable of modifying the expression of mottled rind.

The parents used in this study were 75-11 (Figure 1), a dark green mottled melon, and 'Supersweet' (Figure 2), a nonmottled melon with dark green stripes on a very light green background. F_1 melons were nonmottled. The (75-11 x 'Supersweet') F_2 population produced 137 nonmottled melons and 86 mottled melons (Table 11). The F_2 and backcross frequencies were subjected to a chi-square test for goodness of fit to Weetman's (21) single gene model assuming complete dominance for nonmottled rind. The F_2 population exhibited poor fit ($p = <0.001$) to Weetman's model, however, backcross populations closely agreed ($p = 0.74$, $p = 0.12$) with expected values (Table 11).

Since the F_2 population did not fit a 3:1 model, both the F_2 and backcross populations were fit to a genetic model of nine nonmottled to seven mottled melons. Such a model would be expected if the trait was controlled by two genes and both dominant alleles were required for expression of the dominant nonmottled trait. The results of this test indicate that the F_2 population fits this model ($p = 0.12$). Backcrossing to the dominant parent, 'Supersweet', produced populations which agree with the expected genetic ratios, however, populations derived from backcrossing

Table 11. Distribution of mottled and nonmottled melons in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Mottled melon phenotypes: Observed — Nonmottled	Observed — Mottled	Expected[a] — Nonmottled	Expected[a] — Mottled	Model	X^2	P
75-11 (P_1)	39	0	100	0	100			
Supersweet (P_2)	25	100	0	100	0			
(P_2 x P_1)	24	100	0	100	0			
(P_1 x P_2)	18	100	0	100	0			
(P_1 x P_2) F_2	223	61	39	75	25	3:1	21.88	<0.001
P_1 x (P_1 x P_2)	213	48	52	50	50	1:1	0.11	0.74
(P_1 x P_2) x P_1	6	67	33	50	50	1:1	0.25	0.62
P_2 x (P_1 x P_2)	110	100	0	100	0	1:0		
(P_1 x P_2) x P_2	130	100	0	100	0	1:0		

[a]Expected ratios if nonmottled melons are conditioned by the presence of a single dominant gene (3:1).

to the recessive parent, 75-11, do not agree with the expected ratios (Table 12).

Crosses were made between 75-11 and ten commercially available cultivars (Table 1). All of the resulting F_1 populations with the exception of ('Golden Midget' x 75-11) were nonmottled (Table 13). ('Golden Midget' x 75-11) F_1 plants produced melons which possess the dark green mottling of 75-11 (Figure 8.). 'Golden Midget' is characterized by a light green rind that turns yellow upon maturity.

In this study, mottling appears to be a recessive trait when 75-11 is crossed to most cultivars. However, the presence of mottling in ('Golden Midget' x 75-11) F_1 melons indicates that mottling can also be a dominant trait. The genetic factor that suppresses mottling in most F_1's in this study appears to be absent in 'Golden Midget'.

Weetman's triple allele model

Weetman (21) has proposed that the color locus is in fact a triple allelic series which controls color intensity and stripe appearance. The triple alleles would be G for dark green, g^s for striping, and g for light green rind color. Dark green rind would be dominant to both striped rind and light green rind, and striped rind would be dominant to light green rind. Following this model the genotype for dark green 75-11 (Figure 1) would be GG while striped 'Supersweet' (Figure 2) would be $g^s g^s$ genotypically. Since the F_1 would be heterozygous Gg^s with G being dominant to g^s the F_1 phenotype would be solid dark green. However, both F_1 populations segregated to produce solid dark green melons and medium green melons with dark green stripes (Figures 3 and 4). These phenotypes

Table 12. Distribution of mottled and nonmottled melons in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Phenotypic frequencies in percent — Observed — Nonmottled	Observed — Mottled	Expected[a] — Nonmottled	Expected[a] — Mottled	Model	X^a	P
75-11 (P_1)	39	0	100	0	100	0:1		
Supersweet (P_2)	25	100	0	100	0	1:0		
(P_2 x P_1)	24	100	0	100	0	1:0		
(P_1 x P_2)	18	100	0	100	0	1:0		
(P_1 x P_2) F_2	223	61	39	56	44	9:7	2.43	0.12
P_1 x (P_1 x P_2)	213	48	52	25	75	1:3	181.50	0.00
(P_1 x P_2) x P_1	6	67	33	25	75	1:3	3.00	0.08
P_2 x (P_1 x P_2)	110	100	0	100	0	1:0		
(P_1 x P_2) x P_2	130	100	0	100	0	1:0		

[a]Expected ratio if nonmottled melons are conditioned by the presence of two dominant genes, (9:7).

Table 13. Mottled and nonmottled phenotypes of commercial watermelon cultivars and F_1 populations grown in 1978

Plant population	Mottled phenotype	
	Nonmottled	Mottled
75-11		X
Golden Midget	X	
Golden Midget x 75-11		X
Desert King	X	
Desert King x 75-11	X	
Charleston Gray	X	
Charleston Gray x 75-11	X	
Stone Mountain	X	
Stone Mountain x 75-11	X	
Sugar Baby	X	
Sugar Baby x 75-11	X	
Winter Queen	X	
Winter Queen x 75-11	X	
Klondike	X	
Klondike x 75-11	X	
Congo	X	
Congo x 75-11	X	
Golden Honey	X	
Golden Honey x 75-11	X	

suggest that the dominance of the dark green allele is suppressed at times to allow for the expression of the heterozygous medium green condition. F_1 plants used to produce F_2 and backcross populations produced medium green melons with dark green stripes.

Using Weetman's genetic model, the (75-11 x 'Supersweet') F_2 population would segregate to produce three solid dark green melons to one striped melon. Modifying the model to allow for the expression of the heterozygous condition, a genetic ratio of 1 solid dark green:2 medium green with stripes:1 light green striped melon might be expected. The F_2 population produced 58 solid dark green, 117 medium green striped, and 48 light green striped melons. These data agree closely ($p = 0.90$) with a 1:2:1 genetic ratio (Table 14). Two backcross populations support the genetic model, however, two backcross populations (75-11 x (75-11 x 'Supersweet')) and ('Supersweet' x (75-11 x 'Supersweet')) do not (Table 14).

In summary, Weetman's (21) triple allele model may be used to explain the observed data. However, the data can be explained equally well by the modified triple allele model, the single dominant gene for striping model, and the single incompletely dominant gene for background color model (Tables 7, 9, and 14). However, the phenotypic appearance of some of the field grown parental and F_1 populations can not be explained using the triple allele model (Table 15).

'Charleston Gray' is a netted light green melon with no stripes being present (Figure 13). Using the triple allele model, 'Charleston Gray' would have a genotype of *gg* while the ('Charleston Gray' x 75-11) F_1 would have a genotype of *Gg* and be solid dark green. However, F_1 melons were medium green (Figure 14).

Table 14. Distribution of stripe pattern and background color in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant populations	No. of plants	Stripe and background color phenotypes — Observed: Dark green	Observed: Medium green stripe	Observed: Light green stripe	Expected[a]: Dark green	Expected[a]: Medium green stripe	Expected[a]: Light green stripe	Model	X^2	P
75-11 (P_1)	39	100	0	0	100	0	0			
Supersweet (P_2)	25	0	0	100	0	100	0			
(P_2 x P_1)	24	50	50	0	0	100	0			
(P_1 x P_2)	22	50	50	0	0	100	0			
(P_1 x P_2) F_2	223	26	52	22	25	50	25	1:2:1	0.21	0.9
P_1 x (P_1 x P_2)	213	77	23	0	50	50	0	1:1:0		
(P_1 x P_2) x P_1	6	50	50	0	50	50	0	1:1:0		
P_2 x (P_1 x P_2)	110	0	64	36	0	50	50	0:1:1		
(P_1 x P_2) x P_2	130	0	49	51	0	50	50	0:1:1		

[a]Expected ratios are based on Weetman's triple allelic model for rind color and pattern modified to allow the genotype Gg^s to express both dark green color and stripes.

Table 15. Striped background color phenotypes for commercial watermelon cultivars and F_1 populations grown in 1978

Plant population	Rind phenotype	
	Stripe	Background Color
75-11	no	dark green
Desert King	no	light green
Desert King x 75-11	no	dark green
Charleston Gray	no	light green
Charleston Gray x 75-11	no	medium green
Golden Midget	yes	yellow
Golden Midget x 75-11	no	dark green
Stone Mountain	no	light green
Stone Mountain x 75-11	no	dark green
Sugar Baby	yes	dark green
Sugar Baby x 75-11	no	dark green
Winter Queen	yes	light green
Winter Queen x 75-11	yes	medium green
Klondike	yes	light green
Klondike x 75-11	yes	medium green
Congo	yes	medium green
Congo x 75-11	yes	dark green
Golden Honey	yes	medium green
Golden Honey x 75-11	yes	dark green

'Winter Queen' is a light green melon with stripes of the same color (Figure 15). The genotype of this melon could be either $g^s g^s$ or gg depending on whether the classification is based on color or stripe. If the genotype is assumed to be $g^s g^s$, the F_1 genotype would be Gg^s which should produce a solid dark green melon. If the heterozygote is expressed, the phenotype would be medium green with darker stripes. If the genotype is assumed to be gg, the F_1 genotype would be Gg or solid dark green. However, the actual F_1 melon phenotype was medium green with darker green stripes (Figure 16).

'Klondike' is a light green melon with dark green stripes (Figure 17). The genotype of this melon should be $g^s g^s$. The resulting ('Klondike' x 75-11) F_1 population should possess the genotype Gg^s and produce a solid dark green melon. The F_1 population actually produced medium green melons with dark green stripes. The observed phenotype suggests incomplete dominance for dark green color as well as dominance for stripes (Figure 18).

'Congo' is a medium green melon with dark green stripes (Figure 11). The genotype of this melon would be $g^s g^s$. The expected ('Congo' x 75-11) F_1 genotype would be Gg^s producing a solid dark green phenotype. The observed F_1 phenotype was dark green and striped (Figure 12). Dominance for dark green color and stripes is observed in this cross.

'Golden Honey' is a medium green melon with darker stripes. The genotype for 'Golden Honey' would be $g^s g^s$. The expected ('Golden Honey' x 75-11) F_1 genotype would be Gg^s which should produce a solid dark green phenotype. The observed F_1 was dark green with stripes.

Weetman's triple allele model does not explain the appearance of stripes in many of the observed F_1 populations. The model also fails to account for the wide variation found within phenotypic classes. For example 'Congo', 'Winter Queen', 'Klondike', 'Golden Honey', and 'Sugar Baby' may all be considered striped melons. The model suggests the genotype $g^s g^s$. However, the genotype does not explain the three distinctive types of striping present in these five watermelon cultivars. The model also fails to account for the various shades in color of both stripe and background since stripe color ranges from very light green to dark green and background color ranges from very light green to medium green.

In contrast Weetman's (21) genetic model explains other F_1 phenotypes quite well. 'Desert King' is a very light green melon with no stripes (Figure 5). Using Weetman's triple allele model, 'Desert King's' genotype would be *gg*. The genotype of the ('Desert King' x 75-11) F_1 would be *Gg*, or dark green. The observed ('Desert King' x 75-11) F_1 melons were solid dark green (Figure 6).

'Stone Mountain' is a light green melon with darker netting and no stripe (Figure 9). The genotype of 'Stone Mountain' would be *gg* and the ('Stone Mountain' x 75-11) F_1 genotype would be *Gg*. The expected phenotype of the F_1 would be solid dark green. The observed F_1 phenotype was solid dark green (Figure 10).

'Golden Midget' is a melon that turns from medium green to bright yellow upon maturity (Figure 7). The genotype of this melon is not explained by Weetman's model, but it is assumed to be *gogo* for golden yellow as described by Barnham (1). If this allele operates at the *G*

locus ('Golden Midget' x 75-11) F_1 should be solid dark green. The observed F_1 population was dark green (Figure 8).

'Sugar Baby' is a dark green melon that has visible stripes early in its development but not at maturity. Weetman's triple allelic model does not explain this phenotypic change. However, assuming that the phenotype of the melon could be $g^s g^s$ with a modifier gene present that masks stripe at maturity, the genotype of ('Sugar Baby' x 75-11) F_1 would be Gg^s. Based on this reasoning, the expected phenotype would be solid dark. This phenotype was observed.

Recombination Tests

Tests of independence were made to determine if the traits, background color, striping, and mottling were independently assorted. Tests were made between the following combinations of traits: background color and striping, background color and mottling, and striping and mottling.

Background color and striping

In the (75-11 x 'Supersweet') F_2 population background color is controlled by a single incompletely dominant gene. Striping is controlled by a single dominant gene. Combining these two models and comparing the observed and expected values a chi-square value of 75.63 ($p = <0.001$) was found (Table 16). The model for background color was changed to assume single dominant gene control. Comparing observed and expected values a chi-square value of 21.46 ($p = <0.001$) was produced (Table 17). A second test of independence, using orthogonal contrasts, was applied to the data. Orthogonal contrasts for background color and striping produced nonsignificant chi-square values of 1.44 and 0.12 respectively

Table 16. Chi-square test of independence for the traits background color and stripe in watermelon

Stripe phenotype	Background color phenotype[a] Dark green Observed:Expected[b]	Medium green Observed:Expected[b]	Light green Observed:Expected[b]	Total[c]
Stripe	24:42	93:83	48:42	165:167
Non-stripe	40:14	18:28	0:14	58:56
Total[d]	64:56	111:111	48:56	223:223

[a] $X^2 = 75.63$, DF = 5, P = <0.001

[b] Expected ratio if background color is determined by a single incompletely dominant gene (1:2:1) and stripe is controlled by a single completely dominant gene (3:1).

[c] $X^2 = 0.095$, DF = 1, P = 0.76

[d] $X^2 = 2.86$, DF = 2, P = 0.24

Table 17. Chi-square test of independence for the traits stripe and background color in watermelon

Stripe phenotype	Background color phenotype[a] Dark green Observed:Expected[b]	Light green Observed:Expected[b]	Total[c]
Striped	117:125	48:42	165:167
Non-striped	58:42	0:14	58:56
Total[d]	175:167	48:56	223:223

[a] $X^2 = 21.46$, DF = 3, P = <0.01.

[b] Expected ratio if each trait is controlled by a single completely dominant gene (3:1).

[c] $X^2 = 0.10$, DF = 1, P = 0.76.

[d] $X^2 = 1.52$, DF = 1, P = 0.22.

($p = 0.23$ and 0.73) (Table 18). The orthogonal contrast for recombination produced a chi-square of 20.13 ($p = <0.001$). Such a value suggests that the number of melons in each recombinant class differ significantly from what would be expected if independent assortment had occurred. The nonstriped light green class is not found in the F_2 population. The absence of this phenotype could be caused by incomplete gamete transmission, linkage, or the presence of a multiple allelic series rather than a series of independent loci.

Background color and mottled rind

Mottled rind is controlled by two epistatis genes in the (75-11 x 'Supersweet') F_2 population. The genetic models for mottled rind and background color were combined to determine the expected frequencies for each phenotypic class. When the dominance of dark green background color was considered to be incomplete, the chi-square value for a test of independence of mottled rind and background color was 66.17 ($p = <0.001$) (Table 19). This value indicates that the genes have not recombined in the expected proportions. The dark green nonmottled, medium green mottled, and light green nonmottled classes were smaller than expected. The dark green mottled and the light green nonmottled class were larger than expected. When the medium and dark green classes were combined to form the dark green class, a chi-square value of 7.3 ($p = 0.06$) was found indicating that recombination occurred as expected (Table 20).

Striping and mottled rind

A test of independence was made between the traits mottled rind and striping. A chi-square value of 28.8 ($p = <0.01$) was found (Table 21)

Table 18. Recombination between background color and stripe in watermelon

Contrast[a]	DF	X^2	P
Dark green vs. light green	1	1.44	0.23
Stripe vs. nonstripe	1	0.12	0.73
Recombination	1	20.13	<0.001
Total	3	21.69	0.01

[a]Orthogonal contrasts are based on expected values produced when stripe and background color are each controlled by single dominant genes (3:1).

Table 19. Chi-square test of independence for the traits mottling and background color in watermelon

Mottled phenotype	Background color phenotype[a] Dark green Observed:Expected[b]	Medium green Observed:Expected[b]	Light green Observed:Expected[b]	Total[c]
Non mottled	14:31	87:63	36:31	137:125
Mottled	50:24	24:50	12:24	86:98
Total[d]	64:55	111:113	48:55	223:223

[a] $X^2 = 66.19$, DF = 5, P = <0.001.

[b] Expected ratio if background color is controlled by a single incompletely dominant gene (1:2:1) and mottling is controlled by two epistatic genes (9:7).

[c] $X^2 = 2.62$, DF = 1, P = 0.10.

[d] $X^2 = 2.86$, DF = 2, P = 0.24.

Table 20. Chi-square test of independence for traits mottling and background color in watermelon

Mottled phenotype	Background color phenotype[a] Dark green Observed:Expected[b]	Light green Observed:Expected[b]	Total[c]
Nonmottled	101:94	36:31	137:125
Mottled	74:74	12:24	86:98
Total[d]	175:168	48:55	223:223

[a] $X^2 = 7.30$, DF = 3, P = 0.06.

[b] Expected ratio if background color is controlled by a single completely dominant gene (3:1) and mottling is controlled by two epistatic genes (0:7).

[c] $X^2 = 2.62$, DF = 1, P = 0.23.

[d] $X^2 = 1.18$, DF = 1, P = 0.27.

Table 21. Chi-square test of independence for the traits stripe and mottling in watermelon

Striped phenotype	Mottled phenotype[a] Nonmottled Observed:Expected[b]	Mottled Observed:Expected[b]	Total[c]
Striped	118:95	47:74	165:169
Nonstriped	19:30	39:24	58:54
Total[d]	137:125	86:98	223:223

[a] $\chi^2 = 28.80$, DF = 3, P = <0.01.

[b] Expected ratio if striping is controlled by a single dominant gene (3:1) and mottling is controlled by two epistatic genes (9:7).

[c] $\chi^2 = 0.39$, DF = 1, P = 0.53.

[d] $\chi^2 = 2.62$, DF = 1, P = 0.10.

suggesting the traits are not inherited independently. Orthogonal contrasts were applied to these traits and nonsignificant chi-square values of 2.62 and 0.39 were produced for striping and mottled rind respectively (Table 21). The orthogonal contrast for recombination produced a chi-square value of 26.50 ($p = <0.001$) (Table 22). Both the striped nonmottled and the nonstriped mottled phenotypes were larger than expected while the phenotypes nonstriped nonmottled and nonstriped mottled were both smaller than expected.

Background color, mottled rind, and striping

Attempts were made to combine the three traits together to see if the pooled individual models could explain the F_2 data. As previously suggested, mottled rind is controlled by two epistatic genes which produce, in the case of the (75-11 x 'Supersweet') F_2, a 9:7 ratio of nonmottled to mottled melons. The presence of striping and background color have been shown to be controlled equally well by either Weetman's (21) triple allelic model or a single completely dominant gene controlling striping and a single incompletely dominant gene controlling background color.

To test how well all three traits interact, a model composed of a single completely dominant gene controlling striping, a single incompletely dominant gene controlling background color, and two epistatic genes controlling mottled rind were used to provide expected values for the various phenotypic classes. The observed and expected values were compared (Table 23) and a chi-square value of 172.4 ($p = <0.01$) was produced. The large chi-square value was expected since both the solid light green and dark green striped nonmottled phenotypes were absent and

Table 22. Recombination between stripe and mottling in watermelon

Contrast[a]	DF	X^2	P
Stripe vs. nonstripe	1	1.21	0.27
Mottle vs. nonmottle	1	2.44	0.11
Recombination	1	26.50	<0.001
Total	3	30.15	<0.001

[a]Orthogonal contrasts are based on expected ratios produced when stripe is controlled by a single completely dominant gene (3:1) and mottling is controlled by two epistatic genes (9:7).

Table 23. Chi-square test of independence for the traits background color, stripe, and rind mottling in watermelon

Background color and stripe phenotype	Mottled phenotype		
	Nonmottled Observed:Expected[a]	Mottled Observed:Expected[a]	Total[b]
Dark green - stripe	0:23	24:18	24:41
Medium green - stripe	82:47	11:38	93:85
light green - stripe	36:23	12:18	48:41
Dark green - no stripe	14:8	26:6	40:14
Medium green - no stripe	5:16	13:12	18:28
Light green - no stripe	0:8	0:6	0:14
Total	137:125	86:98	223:223

[a]Expected ratio if background color is determined by a single incompletely dominant gene (1:2:1) while striping and mottling are controlled by a single completely dominant gene (3:1) and two epistatic genes (9:7), respectively.

[b]X^2 = 172.4, DF = 11, P = <0.001.

both the medium green striped nonmottled and the dark green nonstriped mottled phenotypic classes were larger than expected.

Weetman's (21) triple allele model will not explain the results of this study if dark green rind color is completely dominant to stripe. However, if the heterozygous condition, Gg^s, is expressed as a medium green melon with dark green stripes the observed data fit expected values. However, when a 9:7 ratio for mottled rind is used also a chi-square value of 19.06 is produced (Table 24).

Addition of the mottled trait causes poor agreement between observed and expected values. This lack of agreement may be explained if linkage exists between striping and either background color or mottled rind since this linkage between these traits could cause distorted phenotypic frequencies.

Rind Smoothness

Poole (10) found furrowed fruit to be controlled by a single recessive gene. In the study, 75-11 was classified as a smooth melon and 'Supersweet' was classified as a grooved or furrowed melon. Half of the melons produced by the F_1 population were grooved and half had smooth surfaces (Table 25). Explanations provided for rind color segregation in F_1 populations could apply equally well for this trait.

The F_2 plant population was classified as either smooth or grooved based on melon phenotype. Ninety-eight plants produced smooth melons while 125 produced grooved melons. If Poole's (10) model is correct, a 3:1 ratio of smooth to grooved melons would be expected. The data show poor fit ($p < 0.01$) to this model (Table 25). Neither of the backcross

Table 24. Chi-square test of independence for the traits background color, stripe, and rind mottling in watermelon

Background color and stripe phenotype	Mottled phenotype: Nonmottled Observed:Expected[a]	Mottled phenotype: Mottled Observed:Expected[a]	Total[b]
Dark green - solid	19:31	39:24	58:55
Medium green striped	82:63	35:50	117:113
Light green striped	36:31	12:24	48:55
Total	137:125	86:98	223:223

[a]Expected ratio if Weetman's triple allelic model is used and two dominant genes condition the nonmottled trait.

[b]X^2 = 19.06, DF = 5, P = <0.001.

Table 25. Distribution of rind smoothness phenotypes in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Rind smoothness phenotypes — Observed — Smooth	Grooved	— Expected[a] — Smooth	Grooved	Model	X^2	P
75-11 (P_1)	39	100	0	100	0	1:0		
Supersweet (P_2)	25	0	100	0	100	0:1		
($P_2 \times P_1$)	24	71	29	100	0	1:0		
($P_1 \times P_2$)	18	61	39	100	0	1:0		
($P_1 \times P_2$) F_2	223	44	56	75	25	3:1	114.7	<0.01
$P_1 \times (P_1 \times P_2)$	213	60	40	50	50	1:1	9.2	<0.01
$(P_1 \times P_2) \times P_1$	6	33	67	50	50	1:1	0.25	0.62
$P_2 \times (P_1 \times P_2)$	110	21	79	0	100	0:1		
$(P_1 \times P_2) \times P_2$	130	32	68	0	100	0:1		

[a]Expected ratios if rind smoothness is controlled by a single dominant gene (3:1).

populations (75-11 x (75-11 x 'Supersweet')) or ((75-11 x 'Supersweet') x 'Supersweet') agree with the expected values generated by Poole's model.

Since the data did not fit a single gene model, F_2 and backcross populations were compared to values expected if two genes control this trait and both dominant alleles are necessary to condition the dominant, grooved, trait (Table 26). The observed F_2 data fit this model ($p = 1.0$), however, only one small backcross population supports this model.

The poor fit observed could be influenced by several factors including: 1) possible incomplete penetrance or gene instability resulting in a lower frequency of smooth melons than might be expected, 2) the presence of unmodeled modifier genes, 3) possible differences in methods used to classify melon phenotypes between this study and Poole's (8) or 4) the possibility that rind mottling masks or promotes grooved melon phenotypes. A large number of smooth F_2 melons were found to produce grooved cimeras. This suggests the possible presence of an unstable gene.

Table 27 presents the phenotypes of crosses between 75-11 and watermelon cultivars listed in Table 1. Crosses between 75-11 and melons with distinctive grooves, 'Desert King', 'Stone Mountain', 'Winter Queen', 'Congo', and 'Golden Honey', resulted in grooved melons. Some cultivars, 'Charleston Gray', and 'Golden Midget' produced both smooth and grooved melons. The lack of uniformity for this trait within each cultivar may be due to a lack of uniformity during sib-pollination or to unstable genes for grooving.

Table 26. Distribution of rind smoothness phenotypes in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Rind smoothness phenotypes — Observed — Smooth	Grooved	— Expected[a] — Smooth	Grooved	Model	X^2	P
75-11 (P_1)	39	100	0	100	0	1:0		
Supersweet (P_2)	25	0	100	0	100	0:1		
(P_2 x P_1)	24	71	29	0	100	0:1		
(P_1 x P_2)	18	61	39	0	100	0:1		
(P_1 x P_2) F_2	223	44	56	44	56	7:9	0.0	1.0
P_1 x (P_1 x P_2)	213	60	40	25	75	1:3	145.6	<0.001
(P_1 x P_2) x P_1	6	33	67	25	75	1:3	0.17	0.68
P_2 x (P_1 x P_2)	110	21	79	100	0	1:0		
(P_1 x P_2) x P_2	130	32	68	100	0	1:0		

[a]Expected ratios if rind smoothness is controlled by two genes and both dominant alleles are required for grooved rind (9:7).

Table 27. Rind smoothness phenotypes for commercial watermelon cultivars and F_1 populations grown in 1978

Plant population	Rind phenotype	
	Smooth	Grooved
75-11	35	0
Desert King	0	4
Desert King x 75-11	0	5
Charleston Gray	3	2
Charleston Gray x 75-11	6	0
Golden Midget	2	2
Golden Midget x 75-11	1	4
Stone Mountain	0	5
Stone Mountain x 75-11	0	6
Sugar Baby	3	0
Sugar Baby x 75-11	6	0
Winter Queen	0	3
Winter Queen x 75-11	1	5
Klondike	0	4
Klondike x 75-11	0	6
Congo	0	3
Congo x 75-11	0	5
Golden Honey	0	4
Golden Honey x 75-11	0	4

Rind Thickness

Suzuki (18) suggests that a single pair of incompletely dominant genes controls rind thickness. The parents used in his study produced mean rind thickness values of 16.4mm and 5.9mm, respectively. The F_1 population produced a mean rind thickness of 11.2mm. Some variation in thickness was observed in the F_1 population. The F_2 population was classified into three rind thickness groups: 6mm, 10mm, and 12mm. Suzuki (18) observed data produced good fit to a 1:2:1 model.

In this study the rind thickness of both parents was similar to the 10mm class used by Suzuki (18). 75-11 produced a mean rind thickness of 10.5mm and 'Supersweet' produced a mean rind thickness of 8.5mm (Table 28). These cultivars are significantly different when tested at the $p = 0.05$ level. Both F_1 populations, ('Supersweet' x 75-11) and (75-11 x 'Supersweet') produced mean rind thickness readings of 8.7 and 8.9mm respectively. The two F_1 populations were not significantly different for mean rind thickness ($p = 0.50$). In addition both F_1 populations were not significantly different from 75-11 ($p = 0.01$) for this trait.

T-test comparisons suggest there was no significant difference between the F_2 and F_1, (75-11 x 'Supersweet'), populations ($p = 0.50$). Further F_2 rind thickness values did not differ significantly from the arithmetic (9.51mm) or geometric (9.46mm) means of the two parents ($p = 0.5$, $p = 0.5$). In addition the (75-11 x 'Supersweet') F_1 population mean for rind thickness was not significantly different from the arithmetic or geometric mean values mentioned previously ($p = 0.3$, $p = 0.3$). The lack of significant differences between the F_1, F_2, and midparent

Table 28. Distribution of rind thickness in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Rind thickness in millimeters, Upper limit of class 5.9	9.9	13.9	17.9	21.9	Mean
75-11 (P_1)	39	3	28	64	5		10.5 ± 2.2
Supersweet (P_2)	25	4	68	28			8.5 ± 2.3
(P_2 x P_1)	24		64	32	4		8.7 ± 2.1
(P_1 x P_2)	18		50	50			8.9 ± 2.4
(P_1 x P_2) F_2	223	1	54	44	1		9.3 ± 2.1
P_1 x (P_1 x P_2)	213	1	45	48	6		9.9 ± 2.2
(P_1 x P_2) x P_1	6	33	33	34			10.1 ± 2.3
P_2 x (P_1 x P_2)	110	1	43	51	4	1	9.9 ± 2.2
(P_1 x P_2) x P_2	130	17	71	12			9.4 ± 2.2

values would suggest that either there was too much variability within each population to allow the test to discriminate accurately or that additive gene action was present.

Mean rind thickness values and standard deviations for 75-11, the cultivars listed in Table 1, and their respective F_1 populations are listed in Table 29. In crosses to cultivars whose rind thickness was much larger or smaller than 75-11, F_1 populations produced mean rind thickness values which agree with projected midparent values. These results suggest that additive gene effects control rind thickness in watermelon.

Flesh Color

Porter (13) found yellow flesh color was recessive to red flesh color and was controlled by a single recessive gene. Poole (10) also reported on another gene for yellow flesh which was dominant to pink. Shimotsuma (16) suggested that two genes control flesh color, such that *WY* and *Wy* determine white flesh, *wY* yellow flesh, and *wy* red flesh.

The line 75-11 has red-orange flesh color while 'Supersweet' has pink flesh. F_1 populations derived from these parents possess a deep pink-orange flesh color. The F_2 population segregated to produce 56 pink fleshed melons, 62 pink-orange fleshed melons and 105 red-orange fleshed melons (Table 30). The pink-orange and red-orange melons are grouped together and the observed data was to a 3:1 model. The data fit ($p = 0.92$) the model well (Table 31). This would suggest that the presence of orange pigment in the melon flesh color is controlled by a single dominant gene. However, backcross data does not support this control.

Table 29. Mean rind thickness in millimeters for commercial watermelon cultivars and F_1 populations grown in 1978

Plant population	No. of plants	Mean rind thickness in millimeters
75-11	39	10.5 ± 2.5
Desert King	4	15.0 ± 6.6
Desert King x 75-11	4	13.0 ± 2.7
Charleston Gray	5	12.0 ± 0.0
Charleston Gray x 75-11	6	12.0 ± 3.8
Golden Midget	4	4.5 ± 0.6
Golden Midget x 75-11	5	5.8 ± 1.5
Stone Mountain	5	24.4 ± 1.3
Stone Mountain x 75-11	6	15.2 ± 5.8
Sugar Baby	3	6.7 ± 1.2
Sugar Baby x 75-11	6	9.5 ± 1.6
Winter Queen	3	8.0 ± 2.6
Winter Queen x 75-11	6	10.2 ± 2.5
Klondike	4	14.5 ± 4.9
Klondike x 75-11	6	11.3 ± 2.6
Congo	3	12.7 ± 2.1
Congo x 75-11	5	13.8 ± 5.8
Golden Honey	4	12.0 ± 0.8
Golden Honey x 75-11	4	11.5 ± 2.4

Table 30. Distribution of flesh color phenotypes in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Flesh color phenotypes		
		Pink	Pink-orange	Red-orange
75-11 (P_1)	39	0	0	100
Supersweet (P_2)	25	100	0	0
(P_2 x P_1)	24	0	58	42
(P_1 x P_2)	18	0	44	56
(P_1 x P_2) F_2	223	25	29	46
P_1 x (P_1 x P_2)	213	24	29	47
(P_1 x P_2) x P_1	6	17	17	66
P_2 x (P_1 x P_2)	110	24	44	32
(P_1 x P_2) x P_2	130	33	48	19

Table 31. Distribution of flesh color phenotypes in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Flesh color phenotypes — Observed — Pink	Observed — Pink-orange Red-orange	Expected[a] — Pink	Expected[a] — Pink-orange Red-orange	Model	X^2	P
75-11 (P_1)	39	0	100	0	100	0:1		
Supersweet (P_2)	25	100	0	100	0	1:0		
(P_2 x P_1)	24	0	100	0	100	0:1		
(P_1 x P_2)	18	0	100	0	100	0:1		
(P_1 x P_2) F_2	223	25	75	25	75	1:3	0.01	0.92
P_1 x (P_1 x P_2)	213	24	76	0	100	0:1		
(P_1 x P_2) x P_1	6	17	83	0	100	0:1		
P_2 x (P_1 x P_2)	110	24	76	50	50	1:1	15.72	<0.001
(P_1 x P_2) x P_2	130	33	67	50	50	1:1	14.89	<0.001

[a]Expected ratios if orange flesh color is controlled by a single dominant gene (1:3).

Next, the F_2 data were divided into two groups, 118 pink fleshed and 105 red fleshed melons (Table 32). These data fit the 9:7 ratio ($p = 0.92$) expected if two genes control this trait and both dominant alleles are necessary to produce the dominant, pink fleshed, trait. One backcross population, ((75-11 x 'Supersweet') x 75-11) supports this model ($p = 0.17$). The results of this cross suggest that pink flesh color is dominant to red flesh color in watermleon.

The orange pigment found in 75-11 was transferred as a dominant trait in all F_1 populations except ('Sugar Baby' x 75-11) (Table 33). The red flesh of 75-11 was dominant to pink in only two crosses, ('Klondike' x 75-11) and ('Congo' x 75-11). Crosses between 75-11 and two yellow fleshed cultivars, 'Golden Honey' and 'Desert King' produced in pink-orange fleshed melons. These results suggest that in most crosses both pink and orange flesh pigments are dominant to red flesh color.

Flesh Texture

In this study, 75-11 produced a coarse flesh texture while 'Supersweet' produced a fine texture. F_1 plants segregated to produce melons with coarse, medium, and fine textures. F_2 plants were classified into four groups: 109 plants produced coarse textured melons, 13 produced medium textured melons, 93 produced fine textured melons, and 8 produced extra-fine textured melons (Table 34). If the coarse and medium textured melons are combined into one class and the fine and extra-fine textured melons are combined into another class a 9:7 ratio is observed. This suggests that two genes control felsh texture such that both dominant alleles are required to produce coarse flesh texture. F_2 data support

Table 32. Distribution of red and pink flesh color phenotypes in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Flesh color phenotypes Observed Pink	Observed Red	Expected[a] Pink	Expected[a] Red	Model	X^2	P
75-11 (P_1)	39	0	100	0	100			
Supersweet (P_2)	25	100	0	100	0			
(P_2 x P_1)	24	0	100	0	100			
(P_1 x P_2)	18	0	100	0	100			
(P_1 x P_2) F_2	223	53	47	56	44	9:7	2.81	
P_1 x (P_1 x P_2)	213	53	47	75	25	3:1	69.50	<0.001
(P_1 x P_2) x P_1	6	66	34	75	25	3:1	.17	0.68
P_2 x (P_1 x P_2)	110	68	32	100	0	1:0		
(P_1 x P_2) x P_1	130	81	19	100	0	1:0		

[a]Expected ratios is flesh color is controlled by two genes and both dominant alleles are required for pink rind color (9:7).

Table 33. Flesh color phenotypes for commercial watermelon cultivars and F_1 populations grown in 1978

Plant population	Flesh color
75-11	red-orange
Desert King	yellow
Desert King x 75-11	pink-orange
Charleston Gray	pink
Charleston Gray x 75-11	pink-orange
Golden Midget	red-orange
Golden Midget x 75-11	red-orange
Stone Mountain	pink
Stone Mountain x 75-11	pink-orange
Sugar Baby	pink
Sugar Baby x 75-11	pink
Winter Queen	pink
Winter Queen x 75-11	pink-orange
Klondike	pink
Klondike x 75-11	red-orange
Congo	pink
Congo x 75-11	red-orange
Golden Honey	yellow
Golden Honey x 75-11	pink-orange

Table 34. Distribution of flesh texture phenotypes in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Flesh texture phenotypes			
		Coarse	Medium	Fine	Extra-fine
75-11 (P_1)	39	100	0	0	0
Supersweet (P_2)	25	0	0	100	0
($P_2 \times P_1$)	24	92	0	8	0
($P_1 \times P_2$)	18	72	6	22	0
($P_1 \times P_2$) F_2	223	48	6	42	4
$P_1 \times (P_1 \times P_2)$	213	70	5	25	0
$(P_1 \times P_2) \times P_1$	6	67	0	33	0
$P_2 \times (P_1 \times P_2)$	110	58	6	31	5
$(P_1 \times P_2) \times P_2$	130	52	5	41	2

this model ($p = 0.68$); however, backcross data does not ($p < 0.001$) (Table 35). From this model it is apparent that coarse texture is dominant to fine texture. The observed segregation in the F_1 population suggests that both parents may not be homozygous for flesh texture.

Flesh texture phenotypes of sib-pollinated watermelon cultivars and their crosses to 75-11 are listed in Table 36. The only cross that did not produce coarse textured F_1 melons was ('Winter Queen' x 75-11). These melons possess firm texture similar to that of 'Winter Queen' but have external phenotypes distinctly different from either parent. In most crosses coarse flesh texture appears to be dominant; however, some cultivars may possess additional factors which modify the direction of dominance.

Flesh Fiber

No reports on the inheritance of flesh fiber were found in the literature. 75-11 produced a large amount of flesh fiber while 'Supersweet' has only a small amount of flesh fiber. All F_1 melons of the cross (75-11 x 'Supersweet') produced a large amount of fiber while the reciprocal F_1 population of ('Supersweet' x 75-11) produced 2 plants with low fiber melons and 16 plants with high fiber melons. The (75-11 x 'Supersweet') F_2 population segregated to produce melons with large amounts of fiber and melons with small amounts of fiber (Table 37). If two genes control the presence of flesh fiber and the homozygous recessive genotype produced low fiber melon plants, a 15:1 ratio would be expected. The F_2 population fit ($p = 0.17$) this model. Backcross populations involving 75-11 agree with the expected ratios; however, neither of the 'Supersweet'

Table 35. Distribution of flesh texture phenotypes in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Flesh texture phenotypes — Observed — Coarse	Fine	— Expected[a] — Coarse	Fine	Model	X^2	P
75-11 (P_1)	39	100	0	100	0	1:0		
Supersweet (P_2)	25	0	100	0	100	0:1		
(P_2 x P_1)	24	92	8	100	0	1:0		
(P_1 x P_2)	18	78	22	100	0	1:0		
(P_1 x P_2) F_2	223	54	46	56	44	9:7	0.17	0.68
P_1 x (P_1 x P_2)	213	75	25	100	0	1:0		
(P_1 x P_2) x P_1	6	67	33	100	0	1:0		
P_2 x (P_1 x P_2)	110	64	36	25	75	1:3	33.29	<0.001
(P_1 x P_2) x P_2	130	57	43	25	75	1:3	68.27	<0.001

[a]Expected ratios if flesh texture is controlled by two genes and both dominant alleles are required for coarse flesh texture (9:7).

Table 36. Flesh texture phenotypes for commercial cultivars and F_1 populations grown in 1978

Plant population	Flesh texture phenotypes			
	Coarse	Medium	Fine	Extra fine
75-11	39	0	0	0
Desert King	2	2	0	0
Desert King x 75-11	5	0	0	0
Charleston Gray	0	2	3	0
Charleston Gray x 75-11	4	0	2	0
Golden Midget	2	2	0	0
Golden Midget x 75-11	2	2	1	0
Stone Mountain	0	0	5	0
Stone Mountain x 75-11	6	0	0	0
Sugar Baby	0	0	3	0
Sugar Baby x 75-11	1	1	4	0
Winter Queen	0	0	0	3
Winter Queen x 75-11	0	0	0	6
Klondike	1	1	2	0
Klondike x 75-11	5	0	1	0
Congo	0	0	2	1
Congo x 75-11	2	2	1	0
Golden Honey	3	0	1	0
Golden Honey x 75-11	3	0	1	0

Table 37. Distribution of flesh fiber phenotypes in percent for genetic populations derived from 75-11 and 'Supersweet'

		Flesh fiber phenotypes						
		Observed		Expected[a]				
Plant population	No. of plants	High fiber	Low fiber	High fiber	Low fiber	Model	X^2	P
75-11 (P_1)	39	100	0	100	0			
Supersweet (P_2)	25	0	100	0	100			
(P_2 x P_1)	24	92	8	100	0			
(P_1 x P_2)	18	100	0	100	0			
(P_1 x P_2) F_2	223	96	4	94	6	15:1	1.91	0.17
P_1 x (P_1 x P_2)	213	99	1	100	0	1:0		
(P_1 x P_2) x P_1	6	100	0	100	0	1:0		
P_2 x (P_1 x P_2)	110	95	5	75	25	3:1	23.75	<0.001
(P_1 x P_2) x P_2	130	57	43	75	25	3:1	21.48	<0.001

[a]Expected ratios if flesh fiber is controlled by two dominant genes and the presence of either dominant allele conditions high fiber content (15:1).

backcross populations support this genetic model. The ('Supersweet' x 75-11) x 'Supersweet')) population produced fewer low fiber melon plants than were expected while the ((75-11 x 'Supersweet') x 'Supersweet') population produced more low fiber melons than were expected.

The results of crosses between 75-11 and watermelon cultivars other than 'Supersweet' suggest that high flesh fiber is a dominant trait (Table 38).

Seed Coat Color

The inheritance of seed coat color in watermelon has been studied extensively. The most generally accepted model of seed coat color inheritance is the model provided by Poole, Grimball, and Porter (12). They suggest that three major genes affect seed coat color.

The possible phenotypes are *RTW* - flat black, *RTw* - clump (pigment is clumped near the margin, center or hilium of the seed), *RtW* - tan, *Rtw* - white tan tipped, *rtW* - red, and *rtw* - white pink tipped. Two phenotypes *rTW* and *rTw* have not been found in nature; however, it has been suggested by McKay (6) that *rTW* is green. No suggestion has been made for the phenotype of *rTw*. A modifier gene, *d* may be present, but only affects the *RTW* genotype (12). This interaction produces two phenotypes, *RTWD* which is flat black and *RTWd* which is stippled or spotted. The undercoat color of the *RTWd* phenotype has been shown to vary from tan to red in segregating populations (12).

Both 75-11 and 'Supersweet' produce dark brown mottled seeds. If the model above is correct this phenotype could be represented by the genotype *RTWd*. Plants produced by crossing 75-11 with 'Supersweet'

Table 38. Flesh fiber phenotypes of commercial watermelon cultivars and F_1 populations grown in 1978

Plant population	Flesh fiber phenotypes	
	Fiber absent	Fiber present
75-11	0	39
Desert King	3	1
Desert King x 75-11	1	4
Charleston Gray	2	3
Charleston Gray x 75-11	2	4
Golden Midget	0	4
Golden Midget x 75-11	0	5
Stone Mountain	0	5
Stone Mountain x 75-11	0	5
Sugar Baby	2	1
Sugar Baby x 75-11	0	6
Winter Queen	0	3
Winter Queen x 75-11	0	6
Klondike	2	2
Klondike x 75-11	0	6
Congo	1	2
Congo x 75-11	0	5
Golden Honey	4	0
Golden Honey x 75-11	1	3

yielded dark brown mottled seeds. Some segregation was noted in F_2 and backcross populations (Table 39), since tan seeds were produced along with the expected dark brown mottled seeds. Since both parental populations are assumed to be true breeding lines, neither should contain the heterozygous *T* locus. However, if one parent did possess a heterozygous *T* locus the F_2 population could produce both tan seeds and dark brown mottled seeds, but only backcrosses to the heterozygous parent would yield tan seeds in backcross populations. In this study one backcross population derived from each parent produced tan seeds. Since the number of tan seeds is small it is unlikely that both parents were heterozygous for *T*. Instead, the data suggest that the *T* locus may not be completely penetrant; however, it is unclear why penetrance would change in reciprocal backcross populations.

The commercial cultivars that were crossed to 75-11 produced a variety of F_1 seed coat colors (Table 40). The observed parental and F_1 seed coat color phenotypes are accurately explained by the model of Poole, Grimball, and Porter (12). Both 'Golden Midget' and 'Winter Queen' appear to possess a dominant allele at the *d* locus conditioning black seed coat formation. This is evident since crossing each of these cultivars to 75-11 produced F_1 melons with black seed.

Soluble Solids

Research by Suzuki (18) suggests that total soluble solids in watermelon are controlled by five loci, three of which are major incompletely dominant linked genes and two of which are minor modifier genes.

Table 39. Distributuion of seed coat color phenotypes in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Seed coat color phenotypes	
		Dark brown mottled	Tan
75-11 (P_1)	39	100	0
Supersweet (P_2)	25	100	0
(P_2 x P_1)	24	100	0
(P_1 x P_2)	18	100	0
(P_1 x P_2) F_2	223	96	4
P_1 x (P_1 x P_2)	213	90	10
(P_1 x P_2) x P_1	6	100	0
P_2 x (P_1 x P_2)	110	100	0
(P_1 x P_2) x P_2	130	90	10

Table 40. Seed coat color phenotypes for commercial watermelon cultivars and F_1 populations grown in 1978

Plant population	Seed coat color
75-11	Dark brown mottled
Desert King	Dark brown mottled
Desert King x 75-11	Dark brown mottled
Charleston Gray	Dark brown mottled
Charleston Gray x 75-11	Dark brown mottled
Golden Midget	Black
Golden Midget x 75-11	Black
Stone Mountain	White - black tip
Stone Mountain x 75-11	Dark brown mottled
Sugar Baby	Dark brown mottled
Sugar Baby x 75-11	Dark brown mottled
Winter Queen	Black
Winter Queen x 75-11	Black
Klondike	White - Black tip
Klondike x 75-11	Dark brown mottled
Congo	White
Congo x 75-11	Dark brown mottled
Golden Honey	Tan
Golden Honey x 75-11	Dark brown mottled

In this study, data was collected from ripe melons only. Melons produced by the 75-11 population provided a mean soluble solids value of 10.8 percent, while 'Supersweet' melons produced a value of 10.1 percent (Table 41). The two parental values were not significantly different by a t-test ($P = 0.20$). Both F_1 populations, ('Supersweet' x 75-11) and (75-11 x 'Supersweet') produced mean soluble solids readings of 10.6 percent and 10.3 percent respectively. There was no significant difference between the two F_1 populations ($p = 0.50$). Neither F_1 population was significantly different from either 75-11 and 'Supersweet' ($p = 0.50$, $p = 0.50$, $p = 0.10$, and $p = 0.05$). The F_2 population (75-11 x 'Supersweet') produced a mean of 10.5 percent which did not differ significantly from the appropriate F_1 mean ($p = 0.50$). In addition, the F_2 population mean did not differ significantly from the 75-11 mean ($p = 0.30$), the 'Supersweet' mean ($p = 0.30$), or the arithmetic or geometric means of 10.4 percent.

There are not significant differences between the means of the populations. Since the populations are very similar, no genetic model is suggested for genetic control of soluble solids from this study.

In other crosses the mean soluble solids value for 75-11 was larger than similar values for any of the cultivars used (Table 42). The resulting F_1 populations produced mean soluble solids values that fell into two groups, those with values greater than or equal to 75-11, suggesting dominance for high soluble solids, and those with values that fell close to midparent values suggesting additive gene action. From these crosses high soluble solids appear to be controlled by either dominant or additive gene action.

Table 41. Distribution of soluble solids in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Soluble solids in percent[a] upper limits of class 7.9	8.9	9.9	10.9	11.9	12.9	13.9	Mean
75-11 (P_1)	38	3		5	48	39	8	1	10.8 ± 1.0
Supersweet (P_2)	23		21	18	30	22	9		10.1 ± 1.2
(P_2 x P_1)	17			12	21	54	13		10.6 ± 2.4
(P_1 x P_2)	24		17	18	23	42			10.3 ± 1.2
(P_1 x P_2) F_2	136	3	4	16	31	37	8	1	10.5 ± 1.4
P_1 x (P_1 x P_2)	179	4	3	15	41	29	8		10.2 ± 1.9
(P_1 x P_2) x P_1	6			14	33	28	15		10.7 ± 0.8
P_2 x (P_1 x P_2)	109		2	1	28	46	21	2	11.1 ± 1.4
(P_1 x P_2) x P_1	130			9	32	48	10	1	10.9 ± 0.8

[a]Only ripe melons were included.

Table 42. Mean soluble solids for commercial watermelon cultivars and F_1 populations grown in 1978

Plant population	No. of plants	Mean soluble solids in percent
75-11	39	10.8 ± 0.9
Desert King	4	9.5 ± 1.2
Desert King x 75-11	4	10.7 ± 0.3
Charleston Gray	5	9.9 ± 1.0
Charleston Gray x 75-11	6	10.9 ± 0.5
Golden Midget	4	7.6 ± 0.4
Golden Midget x 75-11	5	10.1 ± 0.7
Stone Mountain	5	8.2 ± 1.1
Stone Mountain x 75-11	6	9.9 ± 0.7
Sugar Baby	3	8.8 ± 0.7
Sugar Baby x 75-11	6	11.5 ± 0.9
Winter Queen	3	9.5 ± 0.4
Winter Queen x 75-11	6	10.4 ± 0.8
Klondike	4	10.4 ± 0.8
Klondike x 75-11	6	10.9 ± 0.9
Congo	3	9.9 ± 0.9
Congo x 75-11	5	10.6 ± 0.4
Golden Honey	4	9.4 ± 0.9
Golden Honey x 75-11	4	10.1 ± 0.2

Seed Weight

Weetman (21) found one major dominant gene controls small seed weight. However, his data did not fit a monogenic ratio so he assumed that other factors were involved in determining seed weight.

In this study, 75-11 produced an average seed weight of 0.08 grams while 'Supersweet' produced an average seed weight of 0.05 grams. Both F_1 populations produced an average seed weight of 0.06 grams as did the F_2 population (Table 43). The F_2 population was classified into two groups, those plants producing melons with mean seed weights less than 0.07 grams and those plants that produced mean seed weights greater than 0.07 grams (Table 43). The F_2 population produced 172 small seeded melons and 51 large seeded melons. This observed segregation ratio suggests a single dominant gene might be responsible for small seed weight. Comparing these values to ones expected with single gene control, a good fit ($p = 0.44$) to a 3:1 model was observed. Backcrosses to 'Supersweet', the small seeded parent, resulted in all small seeded melons (Table 43). Backcrossing to 75-11 produced a population which was divided into two groups at 0.07 grams. The observed data did not exhibit a close fit ($p = <0.001$) to the expected 1:1 model.

Table 44 illustrates the seed weights of additional cultivars crossed to 75-11 and the resulting F_1's produced. The results of this study agree with those of Weetman (21). In previous studies, seed size has also been measured in terms of length. Poole, Grimball, and Porter (12) found short (6mm) seeds and long (13mm) seeds were both recessive to medium (10mm) seeds. Using Poole, Grimball, and Porter's (12) classifications, 75-11 would be classified as a long seed while 'Supersweet' would be

Table 43. Distribution of mean seed weight in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Mean seed weight: Observed Small <0.07g	Mean seed weight: Observed Large >0.07g	Mean seed weight: Expected[a] Small <0.07g	Mean seed weight: Expected[a] Large >0.07g	Model	X^2	P
75-11 (P_1)	39	0	100	0	100	0:1		
Supersweet (P_2)	25	100	0	100	0	1:0		
(P_2 x P_1)	24	100	0	100	0	1:0		
(P_1 x P_2)	18	100	0	100	0	1:0		
(P_1 x P_2) F_2	223	77	23	75	25	3:1	0.60	0.44
P_1 x (P_1 x P_2)	213	39	61	50	50	1:1	10.37	<0.001
(P_1 x P_2) x P_1	6	84	16	50	50	1:1	2.67	0.098
P_2 x (P_1 x P_2)	110	100	0	100	0	1:0		
(P_1 x P_2) x P_2	130	100	0	100	0	1:0		

[a]Expected ratios if mean seed weight is controlled by a single dominant gene (3:1).

Table 44. Mean seed weights for commercial watermelon cultivars and F_1 populations grown in 1978

Plant population	No. of plants	Mean seed weight in grams
75-11	39	0.08 ± .006
Desert King	4	0.09 ± .01
Desert King x 75-11	4	0.10 ± .02
Charleston Gray	5	0.08 ± .006
Charleston Gray x 75-11	6	0.10 ± .02
Golden Midget	4	0.03 ± .003
Golden Midget x 75-11	5	0.08 ± .004
Stone Mountain	5	0.11 ± .01
Stone Mountain x 75-11	6	0.10 ± .009
Sugar Baby	3	0.06 ± .02
Sugar Baby x 75-11	6	0.06 ± .005
Winter Queen	3	0.05 ± .0005
Winter Queen x 75-11	6	0.07 ± .003
Klondike	4	0.07 ± .02
Klondike x 75-11	6	0.05 ± .005
Congo	3	0.06 ± .002
Congo x 75-11	5	0.09 ± .006
Golden Honey	4	0.07 ± .09
Golden Honey x 75-11	4	0.08 ± .10

classified as a medium length seed. The F_2 population derived from this cross would be expected to segregate into two groups, 75 percent medium length seeds and 25 percent long length seeds. Further work should be done to determine if there is a correlation between seed length and seed weight.

Days to Harvest

Suzuki (18) found that the number of days from planting to maturity were controlled by four loci, one major completely dominant gene for late maturity and three minor modifier genes. In this study, one ripe melon was harvested from each plant and the number of days to harvest was calculated for each melon (Table 46). The mean number of days to harvest for 75-11 and 'Supersweet' were 134 and 143 days, respectively. However, 75-11 is not significantly earlier ($p = 0.01$) than 'Supersweet' in this study. This may be due to a large variation in the harvest dates for both cultivars. Previous work done with 75-11 and 'Supersweet' has suggested that 75-11 matures an average of a week earlier than 'Supersweet' (Dr. C. V. Hall, Department of Horticulture, Iowa State University, Ames, Iowa, personal communication). Only one population, (75-11 x 'Supersweet') F_2, was carefully evaluated for maturity as it was harvested. A large portion (80%) of the F_2 population was harvested 119 days after planting suggesting that earliness is a dominant trait.

Most watermelon cultivars and F_1 populations listed in Table 46 were harvested within a very short period of time without regard for optimum quality. These data do not accurately reflect normally observed differences in maturity period.

Table 45. Distribution of days to harvest in percent for populations derived from 75-11 and 'Supersweet'

Plant population	No. of[b] plants	Days to harvest[a] upper limit of class 119	124	129	134	139	144	Mean
75-11 (P_1)	8		12.5	37.5			50	134.1 ± 9.8
Supersweet (P_2)	23						100	143.0 ± 0.0
(P_2 x P_1)	6		33	67				124.5 ± 3.5
(P_1 x P_2)	6		33	50			17	127.3 ± 8.4
(P_1 x P_2) F_2	90	80		17	1		2	117.2 ± 6.5
P_1 x (P_1 x P_2)	94		62	32		2	4	123.5 ± 5.6
(P_1 x P_2) x P_1	1				100			136.0 ± 0.0
(P_2 x (P_1 x P_2)	64					75	25	138.2 ± 2.8
(P_1 x P_2) x P_2	82					16	84	142.1 ± 2.2

[a]Number of days from seeding to harvest.

[b]Only ripe melons were included.

Table 46. Mean number of days to harvest for commercial cultivars and F_1 populations grown in 1978

Plant population	No. of plants	Mean days to harvest
75-11	39	136 ± 7.7
Desert King	4	136 ± 0.0
Desert King x 75-11	4	136 ± 0.0
Charleston Gray	5	136 ± 0.0
Charleston Gray x 75-11	6	136 ± 0.0
Golden Midget	4	134 ± 2.0
Golden Midget x 75-11	5	128 ±16.5
Stone Mountain	5	136 ± 0.0
Stone Mountain x 75-11	6	136 ± 0.0
Sugar Baby	3	143 ± 0.0
Sugar Baby x 75-11	6	143 ± 0.0
Winter Queen	3	136 ± 0.0
Winter Queen x 75011	6	136 ± 0.0
Klondike	4	136 ± 0.0
Klondike x 75-11	6	136 ± 0.0
Congo	3	136 ± 0.0
Congo x 75-11	5	134 ± 0.0
Golden Honey	4	134 ± 0.0
Golden Honey x 75-11	4	136 ± 0.0

Maturity Index

In this study, maturity index represents the number of days from fruit set to harvest for ripe melons. The data suggest mean maturity indices of 49.8 days for the 75-11 population and 56.7 days for the 'Supersweet' population (Table 48). The parental maturity indices are significantly different ($p = 0.01$) suggesting 75-11 produced salable melons faster than 'Supersweet'. Both F_1 populations, (75-11 x 'Supersweet') and (75-11 x 'Supersweet') produced mean values of 41.8 days and 42.2 days, respectively. There was no significant difference between these two values ($p = 0.10$). The (75-11 x 'Supersweet') F_1 population took significantly longer to produce mature melons, 42.2 days, than did the F_2 population, 33.9 days ($p = 0.01$). The mean maturity index for the F_2 population was significantly shorter than both the mid-parent mean of 53.3 days and the geometric parental mean of 53.1 days ($p = 0.001$).

The data suggest that the F_2 population produced a mean maturity index that was less than the maturity indices of either parent or the (75-11 x 'Supersweet') F_1 population. This suggests transgressive segregation for early melon production and quicker development time.

Commercial cultivars and F_1 populations were not closely examined to accurately determine their degree of maturity before harvesting. Therefore, some maturity indices listed in Table 49 may be higher or lower than might be expected if melon maturity was accurately determined.

Table 47. Distribution of maturity index in percent for populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Maturity index in days[a] Upper limit of class 29	39	49	59	69	Mean
75-11 (P_1)	8		25	25	50		49.8 ± 9.4
Supersweet (P_2)	23			9	91		56.7 ± 3.4
(P_2 x P_1)	6		33	67			41.8 ± 5.6
(P_1 x P_2)	6		33	50	17		42.2 ± 5.1
(P_1 x P_2) F_2	90	4	88	6	2		33.9 ± 4.7
P_1 x (P_1 x P_2)	94		50	43	7		40.2 ± 5.1
(P_1 x P_2) x P_1	1			100			53.5 ± 5.0
P_2 x (P_1 x P_2)	64		14	86			47.0 ± 0.0
(P_1 x P_2) x P_2	82				97	3	57.3 ± 2.5

[a]Only ripe melons were included.

Table 48. Mean maturity index for commercial watermelon cultivars and F_1 populations grown in 1978

Plant population	No. of plants	Mean maturity index in days
75-11	39	51.7 ± 7.6
Desert King	4	43.0 ± 2.4
Desert King x 75-11	4	54.0 ± 3.9
Charleston Gray	5	52.0 ± 4.2
Charleston Gray x 75-11	6	50.0 ± 2.0
Golden Midget	4	51.8 ± 8.9
Golden Midget x 75-11	5	47.8 ± 9.7
Stone Mountain	5	51.8 ± 3.9
Stone Mountain x 75-11	6	44.3 ± 3.3
Sugar Baby	3	51.0 ± 1.7
Sugar Baby x 75-11	6	46.5 ± 9.2
Winter Queen	3	52.0 ± 0.0
Winter Queen x 75-11	6	52.0 ± 0.9
Klondike	4	45.8 ± 3.9
Klondike x 75-11	6	44.8 ± 2.1
Congo	3	49.7 ± 3.5
Congo x 75-11	5	54.2 ± 2.3
Golden Honey	4	48.0 ± 5.7
Golden Honey x 75-11	4	55.8 ± 3.9

Fruit Shape

Fruit shape is controlled by a single incompletely dominant gene, with round shape being dominant to long (11, 16, 20, 21). A round melon has a length to diameter ratio of 1.00 to 1.25, an intermediate melon has an LD ratio of 1.25 to 1.75, and a long melon has an LD ratio greater than 1.75 (2).

All melons produced by both the 75-11 and 'Supersweet' populations were round (Table 49). The two F_1 populations produced only round melons as did the (75-11 x 'Supersweet') F_2 population. Only round melons were produced in backcrosses involving 75-11. However, in backcrosses involving 'Supersweet' one percent of the melons were of an intermediate fruit shape. Since there was no segregation for fruit shape in the F_2 population, no genetic model is proposed for this study. The two backcross melons of intermediate shape produced LD ratios of 1.35 and 1.33 respectively. Both of these melons are very close to being round and do not represent a major deviation from the expected round shape.

In crosses made between 75-11 and the cultivars listed in Table 1, two of the resulting F_1 populations were of a shape intermediate between the two parents (Table 50). Both 'Congo' and 'Charleston Gray' are long melons with LD ratios of 1.8 and 2.2 respectively. F_1 populations derived by crossing each with 75-11 produced intermediate melons with LD ratios of 1.3 and 1.5 respectively. These two crosses suggest incomplete dominance for round shape.

Table 49. Distribution of fruit shape as measured by length-diameter ratios in percent for populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Length-diameter ratios Upper limit of class Round 1.24	Intermediate 1.75
75-11 (P_1)	39	100	0
Supersweet (P_2)	25	100	0
$P_2 \times P_1$	24	100	0
$P_1 \times P_2$	18	100	0
$(P_1 \times P_2)\ F_2$	223	100	0
$P_1 \times (P_1 \times P_2)$	213	100	0
$(P_1 \times P_2) \times P_1$	6	100	0
$P_2 \times (P_1 \times P_2)$	110	99	1
$(P_1 \times P_2) \times P_2$	130	99	1

Table 50. Length-diameter (LD) ratios for commercial watermelon cultivars and F_1 populations grown in 1978

Plant population	No. of plants	Mean LD ratio
75-11	39	1.08 ± 0.07
Desert King	4	1.10 ± 0.09
Desert King x 75-11	4	1.16 ± 0.02
Golden Midget	4	1.12 ± 0.12
Golden Midget x 75-11	5	1.09 ± 0.07
Stone Mountain	5	1.09 ± 0.09
Stone Mountain x 75-11	6	1.11 ± 0.12
Sugar Baby	3	1.01 ± 0.12
Sugar Baby x 74-11	6	1.10 ± 0.02
Winter Queen	3	1.05 ± 0.09
Winter Queen x 75-11	6	1.04 ± 0.03
Golden Honey	4	1.30 ± 0.40
Golden Honey x 75-11	4	1.08 ± 0.06
Congo	3	1.80 ± 0.03
Congo x 75-11	5	1.30 ± 0.20
Charleston Gray	5	2.18 ± 0.09
Charleston Gray x 75-11	6	1.50 ± 0.09

Melon Density

Melon density was calculated by dividing the weight of each watermelon in grams by its volume in cubic centimeters. In this study the 75-11 population produced melons with a mean density of 0.12gm/cm^3 while the 'Supersweet' population produced melons with a mean density of 0.14gm/cm^3. These two mean densities were not significantly different when compared by a t-test at the $p = 0.01$ level. Reciprocal F_1 populations showed no differences for this trait. The (75-11 x 'Supersweet') F_2 population produced a mean density of 0.13gm/cm^3 as did the backcross populations (Table 51).

The mean densities of the F_1 populations are not significantly different from the mean densities of either 75-11 or 'Supersweet' when compared by a t-test at the $p = 0.01$ level. The data suggest that melon density is fairly uniform in these populations.

The densities of other parental and F_1 populations grown in 1978 are found in Table 52. Although the external phenotypes of these melons vary significantly, it appears that melon density does not vary greatly.

Table 51. Distribution of fruit density in percent for genetic populations derived from 75-11 and 'Supersweet'

Plant population	No. of plants	Fruit density in gm/cm^3 upper limit of class .079	.089	.099	.109	.119	.129	.139	.149	.159	.169	.179	.189	Mean
75-11 (P_1)	39		3	6	6	20	47	15	3					0.12 ± 0.02
Supersweet (P_2)	25					5	10	85						0.14 ± 0.02
(P_2 x P_1)	24					25	43	22	9					0.13 ± 0.01
(P_1 x P_2)	18		12	6	6	6	58	12						0.12 ± 0.02
(P_1 x P_2) F_2	223	1	2	1	3	14	28	30	15	3	1	1	1	0.13 ± 0.02
P_1 x (P_1 x P_2)	213	1	1		1	8	22	26	21	13	5	2		0.13 ± 0.02
(P_1 x P_2) x P_1	6						33	33	34					0.13 ± 0.01
P_2 x (P_1 x P_2)	110		1	1		3	20	44	29	2				0.13 ± 0.01
(P_1 x P_2) x P_2	130		1	1	1	5	44	38	7		1			0.13 ± 0.01

Table 52. Mean fruit densities for commercial watermelon cultivars and F_1 populations grown in 1978

Plant population	No. of plants	Mean fruit density[a] in gm/cm^3
75-11	39	0.12 ± 0.02
Desert King	4	0.13 ± 0.01
Desert King x 75-11	4	0.13 ± 0.02
Charleston Gray	5	0.14 ± 0.04
Charleston Gray x 75-11	6	0.13 ± 0.01
Golden Midget	4	0.10 ± 0.03
Golden Midget x 75-11	5	0.12 ± 0.02
Stone Mountain	5	0.11 ± 0.03
Stone Mountain x 75-11	6	0.13 ± 0.02
Sugar Baby	3	0.14 ± 0.03
Sugar Baby x 75-11	6	0.13 ± 0.01
Florida Giant	2	0.12 ± 0.01
Florida Giant x 75-11	1	0.12 ± 0.01
Winter Queen	3	0.13 ± 0.01
Winter Queen x 75-11	6	0.13 ± 0.04
Golden Honey	4	0.11 ± 0.06
Golden Honey x 75-11	4	0.12 ± 0.02
Klondike	3	0.14 ± 0.03
Klondike x 75-11	5	0.13 ± 0.01

[a]Density was obtained by solving the following formula, $D = W/(4/3\ \pi\ AB^2)$, where A equals melon length in centimeters, B = melon width in centimeters, and W = melon weight in grams.

CONCLUSIONS

In this study, light weight fruit appears to be dominant to heavy weight fruit which agrees with the findings of Weetman (21), Poole and Grimball (11), and Suzuki (18). Dark green rind color was found to be controlled by a single recessive gene. In contrast, Weetman (21) found one completely dominant gene controls dark green color but Porter (13) found the degree of dominance varies. Mottled rind appears to be controlled by two epistatic genes in the F_2 populations produced for this study. However, Weetman (21) found mottled rind to be controlled by a single recessive gene. The data suggest striping was controlled by a single completely dominant gene. McKay (6) and Shimotsuma (16) have reported similar control for striping, however, Weetman (21) found the degree of dominance for striping to be variable.

Weetman's (21) triple allele theory explained the phenotypic segregation of the F_2 population. However, it did not explain the appearance of other F_1 rind phenotypes. The following combinations of traits when tested for recombination yielded significant chi-square values: background color and striping, background color and mottled rind, and mottled rind and striping. The data suggest that linkage may be present between these traits. Further attempts to combine these traits suggest that the observed F_2 phenotypic frequencies cannot be explained by combining genetic models for background color, striping, and mottled rind. In addition, the combination of Weetman's (21) triple allelic series and digenic control for mottled rind did not fully explain the observed data.

Rind smoothness appears to be controlled by two epistatic genes with grooves being the dominant trait. In contrast, Poole (10) found grooved rind to be controlled by a single recessive gene.

There were no significant differences between the F_1, F_2, and mid-parent values for rind thickness suggesting that either a large amount of variability reduced the precision of statistical tests or that additive gene action was present. Suzuki (18) suggested that a single pair of incompletely dominant genes control rind thickness.

The presence of orange pigment in watermelon flesh color was found to be controlled by a single dominant gene. Pink flesh color was also found to be dominant to red flesh.

Coarse flesh texture was found to be dominant to fine texture and controlled by two epistatic genes. Not surprisingly, large amounts of flesh fiber were found to be dominant to small amounts of flesh fiber and controlled by two epistatic genes.

The genetic model for seed coat color proposed by Poole, Grimball, and Porter (12) explained the observed distribution of seed coat colors produced in this study. Light weight seeds were found to be dominant to heavy weight seeds. The trait appears to be controlled by a single dominant gene. Weetman (21) found one major dominant gene controlled small seed weight.

Earliness appears to be dominant in both days to harvest and maturity index. Suzuki (18) found the number of days from planting to maturity was controlled by four loci.

Further areas of research might include a more in-depth study of the mottled rind trait. Reciprocal F_1 populations should be created using a cultivar such as 'Desert King' that produces a solid light green background. F_2 populations should be studied to determine the genetic control. Reciprocal F_1 and F_2 populations should be created between 75-11 and 'Golden Midget' to determine the behavior of mottling in this cross. Samples should be preserved for histological studies. A more in-depth study of melon smoothness and the number of grooves per melon could also be useful.

A number of traits looked at in this study should be reevaluated in a quantitative genetics study. The traits that should be included are fruit weight, rind thickness, soluble solids, days to harvest, maturity index, and melon density. A more objective way of quantifying traits could be helpful. For example, flesh texture could be measured more objectively by a shear press and the bean fiber test could be adapted to watermelon to measure fiber more accurately.

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